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A4936977 A4936978 A4929604 A4929613 A4929613 A4929610 A4923610 A4923610

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Human pro Fruit fly

Abo80084 | Ada55419 | Am25759 | Abo74876 Aau27871

Novel Human

Abg05200

Pseudomon Pseudomon

Title: Perfect score:

Sequence:

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The invention relates to full length GENSET human nucleic acids encoding potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA expression. The sense and antisense nucleic acids may also be used as DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; secreted protein; gene therapy; vaccine; treatment; diagnosis; GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bougueleret L, Jobert S;
                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 21; Page 910-911; 921pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein, SEQ ID NO: 459.
                                              ADP29604
ADP29613
ADP29613
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ADP29607
ABD23210
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06-MAR-2000; 2000US-0187470P
 Dumas Milne Edwards J,
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N-PSDB; AAH64942.
WO200142451-A2.
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                                                                                                                                                                       US-10-057-813-14
861
1 MEHYRKAGSVELPAPSPMPQ......SMPSSSCGPRSRRRARDTRS 163
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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AAG33136 AAG34072 AAG34071

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                                                                                                                                                                                                                   probes in disgnostic assays to detect and quantitate the presence of shiltar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET polypeptide the invention
                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated polypeptides and polynucleotides, useful for preventing, treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders, lymphoid cell disorders, bone degenerative
                                                                                                                                                                              1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                    GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL
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                                                                                                                                                                                                                                                                                                                                                                                                                            neurodegenerative disorder; Jymphoid cell disorder; osteoporosis;
Parkinson's disease; Alzheimer's disease; bone degenerative disorder;
osteoarthritis; periodontal disease; liver fibrosis; viral infection;
fungal infection; bacterial infection; autoimmune disease; diabetes;
atopic dermatitis.
                                                                                                                                      Gaps
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Z, Ghosh M;
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                                                                                                                                                                                                                                                                                                                                                                                                                      genetic disorder; gene mapping; medical imaging; cancer;
                                                                                                                Length 163;
                                                                                                                                      Indels
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R, Wang
                                                                                                               100.0%; Score 861; DB 4; 100.0%; Pred. No. 1.2e-82;
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Yamazaki V, Chen
3 D, Drmanac RT;
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                                                                                                                                                                                                                                                                                                                              ABU00014 standard; protein; 163
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                                                                                                                                                                                                                                                                                                                                                                                              Human novel polypeptide #107.
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                                                                                                                                    Matches 163; Conservative
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Wehrman T, Wang J,
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                                                                                                               Query Match
Best Local Similarity
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                                                                                          Sequence 163 AA
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responsible for genetic disorders or other traits, assessing biodiversity and producing many other types of data and products dependent on DNA and amino acid sequences. They are also useful for preventing, treating or amelicrating medical conditions, such as cancer, neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell disorders, osteoporosis, osteoarthritis, bone degenerative disorders, periodontal disease, liver fibrosis, infections (e.g. viral, fungal or bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis). Sequences ABG99888-ABG9988 and ABU00010-ABU00433 represent human polypeptides of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 861; DB 6;
100.0%; Pred. No. 1.2e-82;
ive 0; Mismatches 0;
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2002US-0406612P.
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2002US-0406640P.
2002US-0406655P.
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Best Local Similarity 100.
Matches 163; Conservative
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29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
29-AUG-2002;
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ADM90988
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2002US-0406666P

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Secreted protein; human; cytokine; cellular proliferation; cell movement; cellular differentiation; immune system regulator; anti-infilammatory; haematopoiesis regulator; tissue growth regulator; tumour inhibitor; reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
                                                                                                                                                                                                                                                                    Extended human secreted protein sequence, SEQ ID NO. 489.
    Bougueleret L, Duclert A, Dumas Milne Edwards J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated human secreted proteins.
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                                                                                                                                     AAY36104 standard; protein; 163
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N-PSDB; AAX97788.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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13-APR-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention relates to novel isolated human polynucleotides and the encoded proteins thereof. Specifically, it refers to proteases, kinases, phosphetases, secreted and transmembrane proteins, as well as the derived peptide fragments, which can be used to develop antibodies and screen for small molecule agonists and antegonists that can modulate their cantivities. The present invention describes polypeptides, polynucleotides, vectors and host cells useful for diagnosing, preventing and treating proliferative disorders, e.g. cancer, disorders of haematopoiesis such as thrombosis and anaemia, cardiovascular disorders, e.g. ischaemic heart disease and acute myocardial infarction, respiratory diseases, e.g. asthma, pneumonia or cystic fibrosis, disorders of the kidney and utinary tract, e.g. chronic renal failure and glomerulopathy, gastrointestinal disorders, e.g. opptic ulcer or cirrhosis, immune disorders, e.g. HIV infection and systemic luque erythematosus, disorders of the endocrine system, e.g. diabetes mellitus, central nervous system disorders, e.g. epilepsy, Alzheimer's disease or amyotropic lateral cativities including cytostatic, anticasthmatic, they exhibit many various activities including cytostatic, anticasthmatic, anticidiammatory, anticativities anticamenic, cardiant, vasotropic, antiasthmatic, anticidiammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nephrotropic, antiulcer, hepatotropic, immunosuppressive, antiallergic, dermatological, antirheumatic, antiarthritic, antidiabetic, antibacterial, anticonvulsant, neuroprotective, nootropic, antipsoriatic, antibacterial, fungicide, antiparasitic and virucidal, such that these polynucleotides can be used for gene therapy purposes and the development of appropriate vaccines. This polypeptide is a human protein of the invention.
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17-SEP-2002; 2002US-0410946P.
17-SEP-2002; 2002US-0410951P.
17-SEP-2002; 2002US-0410953P.
17-SEP-2002; 2002US-0410957P.
17-SEP-2002; 2002US-0410960P.
17-SEP-2002; 2002US-0411019P.
17-SEP-2002; 2002US-0411024P.
17-SEP-2002; 2002US-0411024P.
17-SEP-2002; 2002US-0411034P.
17-SEP-2002; 2002US-0411034P.
17-SEP-2002; 2002US-0411054P.
17-SEP-2002; 2002US-0411052P.
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                                                                       This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a waxiety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify the genes corresponding to the extended cDNAs. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases
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94.4%; Score 813; DB 2; Length 163;
Best Local Similarity 94.5%; Pred. No. 1.4e-77;
Matches 154; Conservative 1; Mismatches 8; Indels
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Claim 9; Page 423-424; 516pp; English
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121 LSRDPLDPNECGYQPPGAPPGLGSMPSSSCGPRSRRARDTRS 163

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proteins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and a method of binding the polypeptide to an antibody. The polymuclactides are useful for expressing the entire secreted proteins which they encode and for distinguishing the human tissues and cells, and for distinguishing between human tissues and cells, and for distinguishing between human tissues and cells, that do not express the polymuclactides comprising the cDNAs. The polymuclactides and polypeptides are useful in forensic procedures or disgnostic procedures to identify individuals with genetic diseases resulting from abnormal expression of the genes corresponding to the cDNAs. The sequences are also useful in gene therapy to control or treat genetic diseases. This sequence are represents a human secreted polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed separation but was obtained in electronic format from USPTO at
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94.5%; Pred. No. 1.4e-77;
ive 1; Mismatches 8; Indels
LXRDPLDPNECGYQPPGAPPGLGSMPSSSCGPRSXKRAXXTRS 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; genetic disease.
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                                                                                                                                                                                            ADP19412 standard; protein; 163 AA.
                                                                                                                                                                                                                                                                                                                                                                                        Human secreted polypeptide #263.
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09-FBB-1999; 99WO-IB000282.
21-UTN-2000; 2000WO-IB000951.
15-SEP-2000; 2000US-00663600.
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Best Local Similarity 94.5
Matches 154; Conservative
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N-PSDB; ADP19007.
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                                                                                                                                RESULT 5
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AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTs) for human secreted proteins expressed in prostate, and encode the proteins given in AAX11716 to AAX11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The concleic acid sequences can be used for products for diagnosis and therapy. The proteins dobtained may have cytokine activity, cell cracking because growth regulating activity, haematopoiesis regulating activity, tissue growth regulating activity, haematopoiesis regulating activity, tissue growth regulating activity, anti-inflammatory activity, tumour inhibition activity on ther activity, anti-inflammatory activity, tumour inhibition activity on the activities. The products can be used in forensic, gene therapy and chromosome mapping procedures can be used in forensic, gene therapy and chromosome mapping procedures sequences can also be used for obtaining corresponding promoter sequences can also be used for obtaining corresponding promoter directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell
                                                                                                                                                                                                                                                                                 Human; secreted protein, EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
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                   0; Indels
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100.0%; Pred. No. 1.6e-34;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                               Human 5' EST secreted protein SEQ ID No: 550.
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                                                                                                                              AAY11950 standard; protein;
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61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymuclectides are useful in gene therapy. A composition containing a polypeptide or polymuclectide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system diseases, such as localised neuropathies and central nervous system diseases, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemoteactic/chemokinetic activity, haemostatic and thrombolytic activity, chemoteactic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemiss and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MEHYRKAGSVEL-----PAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGG 50
                                                                                                                                                                                        peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; hautington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                    Human; nootropic; immunosuppressant; cytostatic; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.4%; Score 339; DB 4; Length 211; 41.9%; Pred. No. 2.5e-27; tive 26; Mismatches 56; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ma Y, (
Xue AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; SEQ ID NO 2118; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     indi V, Chen R,
irman T, Xu C, 1
Drmanac RT;
AAM38973 standard; protein; 211 AA.
                                                                                                                         Human polypeptide SEQ ID NO 2118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-00552317.
2000US-00598042.
2000US-00620312.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-00653450.
2000US-00662191.
2000US-00693036.
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2000US-00488725
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Wang Z, Wehrman T
Goodrich R, Drman
                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAI58129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 211 AA;
                                                                                                                                                                                                                                                                                                                                                                WO200153312-A1
                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-1999;
21-JAN-2000;
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20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-SEP-2000;
                                                                                    22-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                        26-JUL-2001
                                                                                                                                                                                                                                                                              leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT,
Wang J, 1
Zhou P, (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a polypeptide encoded by one of a large number of 5' ESTB derived from mRNAs encoding secreted proteins. The 5' ESTB were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranablated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTB are not well suited for isolating cDNA sequences draw the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTB are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTB are also used in diamonatic from the constant and chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are also used in diagnostic, forensič, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                   Human, 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
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100.0%; Pred. No. 8.8e-34;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Duclert A, Giordano J;
                                                                                                                                                                                                                                                                                              Human secreted protein, SEQ ID NO: 7680.
                                                                                                                                                               AAG03599 standard; protein; 78 AA
                 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-FEB-2000; 2000EP-00200610.
                                                       GRAAGKAVSCAEIVKRRVP
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                                                                                                                                                                                                                                                   06-OCT-2000 (first entry)
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N-PSDB; AAC03605.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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Wang D; Zhao QA;

Ren F, Wa

Qian XB, Yang Y,

13 MENFRKVRSEBAPRGCGAEGGGPGSGPFADLAPGAVHMRVKEGSKIRNLMAFATASMAQP 72

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RESULT 8 AAM38973

Query Match

Matches

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119 TLHILMSLDELPDTIDGLQKPNTSTDFWDGGGAQQQPHPRSQPRHQQQPHKPGAGRGGRP 178
                                                                                                                                                                                                Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                          Arabidopsis thaliana protein fragment SEQ ID NO: 17635.
                                                                                                      AAG16838 standard; protein; 350 AA.
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99US-0135629P.
99US-0136021P.
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99US-0134219P.
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                                                                                                                                                     (first entry)
                         RRRARDTRS 163
                                       99US-01
                                                                                                                                                                                                                        termination sequence.
                                                                                                                                                                                                                                             Arabidopsis thaliana.
                                                                                                                                                    17-OCT-2000
                                                                                                                                                                                                                                                                   EP1033405-A2
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                                                                                                                              AAG16838;
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                                                                                   RESULT 10
                                                                                             AAG16838
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                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16175) and the encoded proteins (ABB5737-ABB72072). The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly
SARHVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSW--VPASPDTGLDP- 107
             62 VWSGSGGGVVKTISCAEVLKRSHP-LYQVTRMAYTSVEEHWKPQM--EGLEEIIVTRQIP 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVP 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----PSSSCGPRS 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154
                                                         developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31;
                                            ----LTVRRHVPAVWVLLSRDPLDPNECGYQPPGAPPGLGSMPSSSCGPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 20022; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27.0%; Score 232.5; DB 4; Length 205; 32.8%; Pred. No. 4.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 20022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 AVWVLLSRDPLDPNECGYOPPGAP----PGLGSM-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Myers EW;
                                                                                                                         ABB64410 standard; protein; 205
                                                                                                                                                                                                                                                                                                                                                                                                      Li PWD,
                                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-0191637P,
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                      Drosophila melanogaster.
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                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75.
N-PSDB; ABL08513.
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                                                                                                                                                                                                                                 pharmaceutical.
                                                                                                                                                                                                                                                                          WO200171042-A2.
                                                                                                                                                                       26-MAR-2002
                                                                                                                                                                                                                   Drosophila;
                                                                                                                                                                                                                                                                                                  27-SEP-2001,
                                                                                                                                                                                                                                                                                                                                                                                                   Venter JC,
                                                                                                                                                 ABB64410;
                                             108
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9908-0139457P.
9908-0139461P.
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9908-0139461P.
9908-0139461P.
9908-014085P.
9908-014086P.
9908-014086P.
9908-0144085P.
9908-0144334P.
9908-014538P.
16-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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22 - JUN - 1999;
23 - JUN - 1999;
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02-AUG-1999
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28-JUN-1
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30-JUN-1
01-JUL-1
01-JUL-1
02-JUL-1
06-JUL-1
08-JUL-1
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61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120 1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS 36; Score 206; DB 3; Length 350; Pred. No. 5.4e-13; 23; Mismatches 65; Indels 23.9%; Score 206; 29.9%; Pred. No. 5 9905-0159299P 9905-0159294P 9905-0159295P 9905-0159330P 9905-0159331P 9905-0159637P 9905-0148684P 9905-0149368P 9905-0149426P 9905-0149722P 9905-0149723P 9905-0149923P 9905-0149930P 9905-0150864P 9905-0150884P 9905-015086P 9905-0151066P 9905-0151080P 9905-0151303P 9905-0151303P 9905-0151303P 9905-015303P 9905-015303P 9905-015303P 9905-015303P 9905-015303P 99US-0156596P. 99US-0157117P. 99US-0157653P. 99US-015865P. 99US-0158029P. 99US-0159584P. 99US-0160741P. 99US-0160767P. 9905-0160981P. 9905-0160989P. 9905-0161404P. 9905-0161406P. 9905-0161359P. 9905-0161361P. 9905-0161361P. 99US-0160768P. 99US-0160770P. 99US-0160814P. 99US-0160815P. 99US-0160980P Local Similarity 29.9 29-SEP-1999; 04-0CT-1999; 06-0CT-1999; 06-0CT-1999; 13-0CT-1999; 13-0CT-1999; 13-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 21-0CT-1999; 21-0CT-1999; 22-0CT-1999; 22-0CT-1999; 22-0CT-1999; 22-0CT-1999; 22-0CT-1999; 26-0CT-1999; 26-0CT-1999; 26-0CT-1999; 26-0CT-1999; 26-0CT-1999; 26-0CT-1999; 26-0CT-1999; 26-0CT-1999; 13-AUG-1999; 13-AUG-1999; 17-AUG-1999; 18-AUG-1999; 20-AUG-1999; 20-AUG-1999; 23-AUG-1999; 23-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999; 310-AUG-1999; 310-AUG-1999; 310-AUG-1999; 310-AUG-1999; 311-SEP-1999; 313-SEP-1999; 32-SEP-1999; 32-SEP-1999; 32-SEP-1999; 33-SEP-1999; 34-SEP-1999; 34-SEP-1999; 35-SEP-1999; 36-SEP-1999; 37-SEP-1999; 37-SEP-1999; 38-SEP-1999; 38-SEP-1999; 38-SEP-1999; 38-SEP-1999; 38-SEP-1999; 38-SEP-1999; 38-SEP-1999; Query Match Best Loca Matches

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990S-0139454P

990S-0139455P

990S-0139455P

990S-0139459P

990S-0139462P

990S-0139462P

990S-0139462P

990S-0139463P

990S-0139463P

990S-0139463P

990S-0139463P

990S-0140333P

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          16-70N-1999

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23-70N-1999

23-70N-1999
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20-JUL-1999;
20-JUL-1999;
20-JUL-1999;
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05-AUG-1999;
06-AUG-1999;
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10-AUG-1999;
11-AUG-1999;
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    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                        121 LSRDPLDPNECGYQPP-----GAPPGLGSMPSSSCGPRSRRAR 159
                                  Arabidopsis thaliana protein fragment SEQ ID NO: 65883.
                                                                                AAG51875 standard; protein; 350 AA.
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990S-0123180P.
990S-012548P.
990S-0126264P.
990S-0126264P.
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990S-0128234P.
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990S-0130891P.
990S-0131449P.
990S-0131419P.
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99US-0137222P.
99US-0137528P.
99US-0137724P.
99US-0138094P.
99US-0138640P.
99US-0138847P.
                                                                                                                                                                                                                               25-FEB-2000; 2000EP-00301439
                                                                                                                18-OCT-2000 (first entry)
                                                                                                                                                                               Arabidopsis thaliana
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GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                            121 LSRDPLDPNECGYQPP------GAPPGLGSMPSSSCGPRSRRAR 159
                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 65844.
                                                                                                                                                                       AAG51847 standard; protein; 350 AA
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990S-0126762P
990S-0128714P
990S-0128714P
990S-0130449P
990S-0130449P
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9905-01342219-
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9905-0134941P-
9905-01353239-
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99US-0123548P.
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99US-0138540P
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                                                                                                                                                                                                                                     (first entry)
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07-JUN-1999;
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28-MAY-1999;
01-JUN-1999;
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        990S-0148684P

990S-0148684P

990S-0149175P

990S-0149172P

990S-0149722P

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990S-0149929P

990S-0149929P

990S-01510684P

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27-AUG-1999;
27-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
31-AUG-1999;
32-SEP-1999;
32-SEP-1999;
32-SEP-1999;
32-SEP-1999;
32-SEP-1999;
32-SEP-1999;
33-AUG-1999;
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PR 13-AUG-1999; 99US-014684P.
PR 13-AUG-1999; 99US-014684P.
PR 16-AUG-1999; 99US-014684P.
PR 20-AUG-1999; 99US-0144912P.
PR 23-AUG-1999; 99US-0149722P.
PR 23-AUG-1999; 99US-0149722P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149902P.
PR 24-AUG-1999; 99US-0149902P.
PR 25-AUG-1999; 99US-0151066P.
PR 25-AUG-1999; 99US-015106P.
PR 25-AUG-1999; 99US-015106P.
PR 25-AUG-1999; 99US-015106P.
PR 26-AUG-1999; 99US-015106P.
PR 26-AUG-1999; 99US-015130P.
PR 26-AUG-1999; 99US-015130P.
PR 27-AUG-1999; 99US-015130P.
PR 27-AUG-1999; 99US-015130P.
PR 28-EPP-1999; 99US-015645P.
PR 28-EPP-1999; 99US-015649P.
PR 28-EPP-1999; 99US-016676P.
PR 28-EPP-1999; 99US-015693P.
PR 28-EPP-1999; 99US-0156

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Query Match 23.9%; Score 206; DB 3; Length 350; Best Local Similarity 29.9%; Pred. No. 5.4e-13; Matches 53; Conservative 23; Mismatches 65; Indels

us-10-057-813-14.rag

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Gaps

36;

65; Indels

23; Mismatches

53; Conservative

Matches

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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up or down-regulated in transgenic plants overagressing the heterodimeric strange transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilisation and/or altered bhotosynthesis, each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/ or carbon metabolism or they function as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transcription factors. This polypeptide sequence is thale cress protein expressed by a gene upregulated 1.3 fold or more in plants overexpressing the E2Fa/DPa transcription factor, given in an exemplification of the
GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
                      Altering plant characteristics, useful for producing plants for enzyme c
pharmaceutical production comprises modifying in a plant, expression of
one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                    Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 778
                                                                           ----GAPPGLGSMPSSSCGPRSRRAR 159
                                                                                                  plant; transgenic; E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
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                                                                                                                                                                                                                 ADN72883 standard; protein; 350 AA
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                                                                           121 LSRDPLDPNECGYQPP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up characteristics. Specifically, it refers to identifying genes that are up care of whom-regulated in transgenic plants overexpresshing the heterodimeric EZFA/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, carly managenic plants for the production of growth regulators, carly manages, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these cach relative to the corresponding wild type plants. Accordingly, these deduction that the stands of the calls or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell and playeptide sequence is thale cress protein expressed by a gene upregulated 1.3 fold or more in plants overexpressing the EZPA/DPa transcription factor, given in an exemplification of the
                                                                                                         ||| || : |::|||:| ||| |: || GRAINKTVIIVELIKRRIPDLHQNTSIGSTDITDTWEPT--EEGLLPLETTRHVSMITIT 111
                                                                                GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS 60
                        Altering plant characteristics, useful for producing plants for enzyme opharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 78.
                                                                                                                                                                        121 LSRDPLDPNECGYQPP------GAPPGLGSMPSSSCGPRSRRAR 159
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LSKIELNTSSVGYQCPIPIELVKPMGDIDYEGREGSPGGRG------RGRGRGR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant; transgenic; E2Pa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
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Score 206; DB 8; Length 350; Pred. No. 5.4e-13;

23.9%;

Best Local Similarity

Query Match

Sequence 350 AA;

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99US-0135629P.
99US-0136021P.
99US-0136032P.
99US-0137528P.
99US-0137528P.
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99US-0145086P.
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24-MAY-1999,
25-MAY-1999,
28-MAY-1999,
01-JUN-1999,
03-JUN-1999,
04-JUN-1999,
06-JUN-1999,
10-JUN-1999,
110-JUN-1999,
 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
                                                                                                             1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS 60
                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                     121 LSRDPLDPNECGYOPP------GAPPGLGSMPSSSCGPRSRRAR 159
                                                                                                                                                 36; Gaps
                            Length 350;
                                            65; Indels
                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 65843.
                        23.9%; Score 206; DB 8; 29.9%; Pred. No. 5.4e-13; ive 23; Mismatches 65
                                                                                                                                                                                                      AAG51846 standard; protein; 356 AA
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99US-0123548P-
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99US-0128234P-
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99US-012845P-
99US-0129845P-
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                                                                                                                                                                                                                                          18-OCT-2000 (first entry)
                                          53; Conservative
                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
                      Query Match
Best Local Similarity
       Sequence 350 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-APR-1999

16-APR-1999

19-APR-1999

21-APR-1999

23-APR-1999

28-APR-1999

30-APR-1999

30-APR-1999

30-APR-1999

66-MAY-1999

65-MAY-1999
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                                          Matches
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PR 02-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-014638P.
PR 04-AUG-1999; 99US-0147102P.
PR 05-AUG-1999; 99US-0147102P.
PR 05-AUG-1999; 99US-0147102P.
PR 05-AUG-1999; 99US-0147102P.
PR 10-AUG-1999; 99US-0147102P.
PR 11-AUG-1999; 99US-0147102P.
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PR 12-AUG-1999; 99US-0147102P.
PR 12-AUG-1999; 99US-0149712P.
PR 12-AUG-1999; 99US-0149712P.
PR 23-AUG-1999; 99US-014972P.
PR 23-AUG-1999; 99US-014978P.
PR 23-ESEP-1999; 99US-014978P.
PR 23-ESEP-1999; 99US-014978P.
PR 23-ESEP-1999; 99US-014978P.
PR 23-ESEP-1999; 99US-014978P.
PR 24-CCT-1999; 99US-0149773P.
PR 13-CCT-1999; 99US-0149773P.
PR 13-CCT-1999; 99US-016909.
PR 24-CCT-1999; 99US-016909.
PR 25-CCT-1999; 99US-0169
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61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120 60 GRAINKTVTIVELIKRRIPDLHQNTSIGSTDITDTWEPT--EEGLLPLETTRHVSMITIT 117 1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS 60 LSRDPLDPNECGYQPP------GAPPGLGSMPSSSCGPRSRRAR 159 Gaps 36; Query Match 23.9%; Score 206; DB 3; Length 356; Best Local Similarity 29.9%; Pred. No. 5.5e-13; Matches 53; Conservative 23; Mismatches 65; Indels : 99US-0161992P. 99US-0161993P. 99US-0162142P. 28-OCT-1999; 28-OCT-1999; 29-OCT-1999; 121 PR PR 셤 ò ઠે 원 ò g

Search completed: January 26, 2005, 15:01:03 Job time : 166.447 secs Adl12363 Human ste Abx52110 Bovine ES Ab115187 Drosophil Ada71938 Rice gene Aaf1938 Rice gene Aaf15097 Trichoder Ab115186 Drosophil Aa136926 Human ner Aba17490 Human ner Aba17490 Human ner Abx5914 cDNA enco Ad51790 Human ner Abx5914 cDNA enco Ad510664 Human mus Acc19059 E. coli 0 Adc100585 Enterohae Adm66939 Murine ad Adm66939 Murine ad Adm66939 Murine ad Adm72182 Thale cre Adm72182 Thale cre Adm72882 Thale cre

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gene; ds; human; cancer; haematopoiesis; thrombosis; anaemia;
cardiovascular disorder; ischaemic heart disease;
w cardiovascular disorder; ischaemic heart disease;
w cute myocardial infarction; respiratory disease; asthma; pneumonia;
cystic fibrosis; chronic renal fallure; glomerulopathy;
w gastrointestinal disorder; peptic ulcer; cirrhosis; immune disorder;
w HIV infection; systemic lupus erythematosus; immune disorder;
w diabetes mellitus; epilepsy; Alzheimer's disease;
w amyotropic lateral sclerosis; skin disorder; psoriasis bacterial;
thrombolytic; antianaemic; cardiant; vasotropic; anticogulant;
thrombolytic; antianaemic; cardiant; vasotropic; antiasthmatic;
antinflammatory; nephrotropic; antiulcer; hepatotropic;
antiarthritic; antidiabetic; anticonvulsant; neuroprotective; nootropic;
antipporiatic; antibacterial; fungicide; antiparasitic; virucidal;
                                                                                                                                                                                                                                                                                                                                                           Human DNA encoding a pharmaceutically useful protein SeqID 590.
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                          ADA71938
ADA71938
AAF15097
ABL15186
AAL36926
ABA16341
ABA17790
ABX59914
AAC3664
AAC3679
ACD19059
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AAC50707
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29-AUG-2002; 2002US-0406611P.
29-AUG-2002; 2002US-0406612P.
29-AUG-2002; 2002US-0406616P.
29-AUG-2002; 2002US-0406656P.
29-AUG-2002; 2002US-0406666P.
17-SEP-2002; 2002US-0410946P.
17-SEP-2002; 2002US-0410951P.
                                                                                                                                                                                                                                                                                                  ADM91197 standard; DNA; 660 BP
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                                             ADM91197;
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000000 00
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Ada 99056 Human sec
Ada 1904 Human sec
Ada 1904 Human sec
Adf 10630 Human sec
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Aax40672 Human sec
Abr41218 Toxicity
Aai59915 Human pol
Aai58129 Human pol
Adq98335 DNA encod
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Adm90779 Human DNA
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Abx05092 Human nov
Aax97788 Extended
                                                              January 31, 2005, 10:10:14; Search time 390 Seconds (without alignments) 6622.347 Million cell updates/sec
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                                                                                                                        1 atggagcactaccggaaagc.......tcgagacacccgatcgtga 492
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        version 5.1.6
- 2005 Compugen Ltd.
                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                      4134886 segs, 2624710521 residues
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Listing first 45 summaries
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ABXC5092
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geneseqn2003ds:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene; ds; human; cancer; haematopoiesis; thrombosis; anaemia; cardiovascular disorder; ischaemic heart disease; asthma; pneumonia; acute myocardial infarction; respiratory disease; asthma; pneumonia; cystic fibrosis; chronic renal failure; glomerulopathy; gastrointestinal disorder; peptic ulcer; cirrhosis; immune disorder; HIV infection, systemic lupus erythematosus; endocrine system; diabetes mellitus; epilepsy; Alzheimer's disease; anticoagulant; fungal; parasitic; viral infection; cytostatic; anticagulant; thrombolytic; antianaemic; cardiant; vasotropic; antiathmatic; thrombolytic; antianaemic; cardiant; vasotropic; antiathmatic; antiinflammatory; nephrotropic; antiucer; hepatotropic; antiathmatic; antipheresic; anticonvulsant; neuroprotective; nootropic; antipporiatic; antibacterial; fungicide; antiparasitic; virucidal;
                                                           349 GGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGGTCCCAGGC
                                                                                                                                                                                                            CCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTGCTG
                                                                                                                                                                                                                                              CTGACACAGGGGTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGGGTGCGCTG
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                                                                                                                                                                                                                                                                                                               CTCAGCCGGGACCCCCTGGACCCCAATGAGTGTGTTACCAACCCCCAGGAGCACCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                               Human DNA encoding a pharmaceutically useful protein SegID 172.
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2002US-0406611P.
2002US-0406612P.
2002US-0406616P.
2002US-0406655P.
2002US-0406666P.
2002US-0410946P.
2002US-0410953P.
2002US-0410957P.
2002US-0410957P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to novel isolated human polynucleotides and the encoded proteins thereof. Specifically, it refers to proteases, kinases, phosphatases, secreted and transmembrane proteins, as well as the derived peptide fragments, which can be used to develop antibodies and screen for small molecule agonists and antagonists that can modulate their cativities. The present invention describes polypeptides, preventing and treating proliferative disorders, e.g. cancer, disorders of and treating proliferative disorders, e.g. cancer, disorders of and treating proliferative disorders, e.g. cancer, disorders of e.g. ischaemic heart disease and acute myocardial infarction, respiratory diseases, e.g. asthma, pneumonia or cystic fibrosis, disorders of the kidney and urinary tract, e.g. chronic renal failure and glomerulopathy, c.g. ischaemic plainter, e.g. chronic renal failure and glomerulopathy, c.g. intary tract, e.g. opptic ulcer or cirrhosis, immune disorders, e.g. HUY infection and systemic lupus erythematosus, disorders of the endocrine system, e.g. diabetes mellitus, central nervous system confisorders, e.g. epilepsy, Alzheimer's disease or amyotropic lateral confisorders, e.g. peptic ulcer or cirrhosis, immune confisorsis, skin disorders, e.g. psoriasis, as well as bacterial, fungal, sclerosis, skin disorders, e.g. psoriasis, as well as bacterial, fungal, continnesmic, antilanaemic, antilanaemic, antilanaemic, antilanaemic, antilanaemic, antilanaemic, antilanaemic, cardiant, vasotropic, antisathmatic, antilanaemic, antilanaemic, antilanaemic, antilanaemic, antisathmatic, antilanaemic, antiparasitic and virucidal, such that these polymucleotides anticonvulsant, neuroprotective, nootropic, antipasedic, antilanaemic can be used for gene therapy purpose and the development of appropriate curvance.

Continged of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New human polynucleotides and polypeptides, useful for diagnosing, preventing and treating proliferative disorders, immune disorders, cardiovascular disorders, or bacterial, fungal, parasitic and viral
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                                                                                                                                                                                                                                                                                                                                                                                     Lee E, Hestir K;
                                                                                                                                                                                                                                                                           FIVE PRIME THERAPEUTICS INC.
RIKEN INST PHYSICAL & CHEM RES.
DNAFORM KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 590; 254pp; English.
17-SEP-2002; 2002US-0410960P.
17-SEP-2002; 2002US-0410962P.
17-SEP-2002; 2002US-0411019P.
17-SEP-2002; 2002US-0411022P.
17-SEP-2002; 2002US-0411024P.
17-SEP-2002; 2002US-0411037P.
17-SEP-2002; 2002US-0411046P.
17-SEP-2002; 2002US-0411046P.
17-SEP-2002; 2002US-0411046P.
                                                                                                                                                                                                                            2002US-0411111P
                                                                                                                                                                                                                                                                                                                                                                             Williams LT, Chu K,
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-257410/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; ADM90988
                                                                                                                                                                                                                               17-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases.
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(DNAF-)
                                                                                                                                                                                                                                                                             (FIVE-)
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potentially secreted proteins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GENSET gene expression. For example, they be used to treat disorders associated with decreased GENSET gene expression by rectifying mutations or deletions in a patient's gene expression by rectifying mutations or deletions in a patient's patients own production of GENSET polypeptides. Conversely, antisense nucleic acid molecules may be administered to down regulate GENSET expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which
                                                                        CTGCACCAGCTCACCAAGCTACGTTTCCTTCAAGACAGAGACAGCTGAGGTCCCAGCCTCA 468
                                                                                                                                              360
                                                                                                                                                                    CCTGACACACAGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTGCTG 528
                                                                                                                                                                                                                                       420
                                                                                                                                                                                                                                                                                       588
                                                                                                                                                                                                                                                                                                                                      GGCCTGGGTTCCATGCCCAGCTCCAGCTGTGGCCCTCGTTCCCGAAAGAAGGGCTCGAGAC 480
                                                                                                                                                                                                                                                                                                                                                                                   GGCCTGGGTTCCATGCCCAGCTCCAGCTGTGGCCCTCGTTCCCGAAGAAGGACGGCTCGAGAC 648
GGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTCCCAGGC 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to full length GENSET human nucleic acids encoding
                                                                                                                                           CCTGACACACAGGGCTAGACCCCCTCACAGTGCGCCGCCCATGTGCCTGCAGTGTGGGGTGCTG
                                                                                                                                                                                                                                                                     CTCAGCCGGGACCCCCTGGACCCCCAATGAGTGTGGTTACCAACCCCCCAGGAGCACCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                       CTCAGCCGGGACCCCCTGGACCCCAATGAGTGTGGTTACCAACCCCCAGGAGCACCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; gene therapy; vaccine; treatment; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO: 218.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 7; Page 772-773; 921pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH64942 standard; cDNA; 894 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-1999; 99US-0169629P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  481 ACCCGATCGTGA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-367870/38.
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349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to novel isolated human polynucleotides and the encoded proteins thereof. Specifically, it refers to proteases, kinases, phosphatases, secreted and transmembrane proteins, as well as the derived composition of the present invention be used to develop antibodies and screen for small molecule agonists and antagonists that can modulate their continuities. The present invention describes polypeptides, preventing and treating proliferative disorders, e.g. cancer, disorders of and treating proliferative disorders, e.g. cancer, disorders of namatopoiesis such as thrombosis and anaemia, cardiovascular disorders, e.g. ischaemic heart disease and acute myocardial infarction, respiratory diseases, e.g. asthma, pneumonia or cystic fibrosis, disorders of kidney and urinary tract, e.g. chronic renal failure and glomerulopathy, gastrointestinal disorders, e.g. opeptic ulcer or cirrhosis, immune disorders, e.g. HIV infection and systemic lupus erythematosus, disorders of the endocrine system, e.g. diabetes mellitus, central nervous system disorders, e.g. peptic disease or amycoropic lateral collectors, skin disorders, e.g. paptic sissasses or amycoropic lateral collectors, skin disorders, e.g. paptic and viral diseases. Accordingly, they exhibit many various collection cardianance antial infammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             169 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polynucleotide is a human DNA sequence encoding a
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100.0%; Pred. No. 5.9e-120;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                             Hestir K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 172; 254pp; English.
                                                                                                                                                                                                            FIVE PRIME THERAPEUTICS INC.
RIKEN INST PHYSICAL & CHEM RES.
                             17-SEP-2002; 2002US-0411024F)
17-SEP-2002; 2002US-0411037F)
17-SEP-2002; 2002US-0411037F]
17-SEP-2002; 2002US-0411052F]
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Matches 492; Conservative
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patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET nucleic acid of
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                                                                                                               Length 894;
                                                                                   Sequence 894 BP; 189 A; 258 C; 255 G; 192 T; 0 U; 0 Other;
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                                                                                                                         Local Similarity 100.
1es 492; Conservative
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                                                          the invention
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Human; gene; ss; genetic disorder; gene mapping; medical imaging; cancer; neurodegenerative disorder; lymphoid cell disorder; osteoporosis; Parkinson's disease; Alzheimer's disease; bone degenerative disorder; osteoarthritis; periodontal disease; liver fibrosis; viral infection; fungal infection; bacterial infection; autoimmune disease; diabetes; atopic dermatitis.
                                                                                                        Human novel polynucleotide #107.
                          standard; cDNA; 1089
                                                                               (first entry)
                                                                               17-JAN-2003
                                                    ABX05092;
                          ABX05092
RESULT
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14-MAR-2002; 2002WO-US005109.

WO200274961-A1

26-SEP-2002

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The invention relates to human polynucleotides and the polypeptides they encode. The polynucleotides and polypeptides are useful in diagnostics, forensics, gene mapping, medical imaging, identification of mutations responsible for genetic disorders or other traits, assessing biodiversity and producing many other types of data and products dependent on DNA and amino acid sequences. They are also useful for preventing, treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders, osteoporosis, osteoarthitis, bone degenerative disorders, periodontal disease, liver fibrosis, infections (e.g. viral, fungal or bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis). Sequences ARX04986-ARX05511 represent human polymoids of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480
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                                                                                                                                                                                                                                                                                                                                                    wew isolated polypeptides and polynucleotides, useful for preventing, treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders, lymphoid cell disorders, bone degenerative disorders, and infections.
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Z, Ghosh N
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                                                                                                                                                   Goodrich R, Asundi V, Zhang J,
Ma Y, Yamazaki V, Chen R, Wang
J, Wang D, Drmanac RT;
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100.0%; Score 492; DB 8; I
Best Local Similarity 100.0%; Pred. No. 6.6e-120;
Matches 492; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; SEQ ID NO 107; 235pp; English.
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                      L5-MAR-2001; 2001US-00810173
                                                                                                                                                                                                                       Wang J,
                                                                                                                                                                                                                                                                                  WPI; 2003-040556/03
                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                      Zhou P,
                                                                                                                                                                                                                                                                                                            P-PSDB; ABU00014
                                                                                                                                                                                   Yang Y,
                                                                                                                                                                                                                    Wehrman T,
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The invention relates to human cDNA sequences that encode human secreted protesins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and a method of binding the polypeptide to an antibody. The polymucleotides are useful for expressing the entire secreted proteins which they encode and for distinguishing
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                                                                                                     CTGCACCAGCTCACCCAAGCTACKTTTCCTTCAAACTGAGGACAGCTGGGTCCCASCCTCA
                                                                                                                                                                                                                                                                   189 GGGTTGGCTCTGGGTCGGTTGGAGGCGCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT
                                                                                GGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTCCCAGGC
                                                                                                                                                               CTGCACCAGCTCACCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGGCTCA
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  GGGTTGGCTCTGGGTCGGTTGGAGGCCGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 311; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted polynucleotide #311.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-DEC-1998; 98WO-IB002122.
09-FEB-1999; 99WO-IB000282.
21-JUN-2000; 2000WO-IB000951.
15-SEP-2000; 2000US-00663600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; cDNA; 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify the genes corresponding to the extended conNas. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases
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                                                                                                                                                                                                                                                                                                   Secreted protein; human; cytokine; cellular proliferation; cell movement; cellular differentiation; immune system regulator; anti-inflammatory; haematopoiesis regulator; tissue growth regulator; tumour inhibitor; reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
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                                                                                                                                          AAX97788 standard; DNA; 884 BP.
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98US-0074121P.
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98US-0096116P.
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481 ACCCGATCGTGA
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13-APR-1998;
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06-APR-2000; 2000WO-US008983 09-APR-1999; 99US-0128703P. 14-JAN-2000; 2000US-0176068P.

WO200061596-A1. 19-OCT-2000

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98.4%; Score 484; DB 12; Length 884;
Best Local Similarity 97.8%; Pred. No. 8.1e-118;
Matches 481; Conservative 8; Mismatches 3; Indels C
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Aricia de contra CTACCTCCTGATACCCTGGAGATGCGGGTCCGAGATGCCAGCAAAATCCGCAACCTACTG 1 ATGGAGCACTACCGGAAAGCTGGCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG GGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 164 GGGCTGGCACTGGATTGGA-GGTGGTGGTGCACGGCATGTGGTTCTCAGGTTCT GGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTCCCAGGC Gercegertecadgeaagecagreacrierecreacarriereaagececereraccegec CTGCACCAGCTCACCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCA Score 385.6; DB 3 Pred. No. 7.9e-92, 0; Mismatches 59 78.4%; Best Local Similarity 87.8 Matches 432; Conservative 44 61 104 121 223 181 Query Match 241 ઠે 셤 ò 엄 ò g ò g ò Human; secreted protein; cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antialergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; cancer; immune disease; allergy; cardiovascular disorder; wound healing; infection; neurological disease; Human secreted protein gene 49 SEQ ID NO:59 AAC95569 standard; cDNA; 1036

21-FEB-2001

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103 120 163 180 222 240 282

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59; Indels

Length 1036;

DB 3;

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Polymucleotide sequences AAC95521 - AAC95570 represent cDNA encoding 50 human secreted proteins AAB52012 - AAB52161. Sequences AAB52062 - CC human secreted proteins AAB52012 - AAB52161. Sequences AAB52062 - CC AAB52103 represent alternative polypeptides encoded by the genes, and camino acid sequences with which they share homology. The genes and proteins have activities dependent on the tissues and cells in which they care expressed. Examples of their activities include cytostatic; immunosuppressive; nootropic, antidiametory; antidiac antiallergic; cimmunosuppressive; nootropic, antifilammatory; antidicer; vulnerary; cc anticonvulsant; antibacterial; antifilammatory; antidicer; vulnerary; cc anticonvulsant; antibacterial; antifilammatory; antiparasitic; and cardiant. The secreted proteins polypeptides, antagonists and agonists may be useful in treating, preventing and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gatcrointestinal tract, cliver, lung, or urogenital. Immune disorders such as Addison's disease, multiple softens, rheumatoid arbritis and ulcerative colitis; cardiovascular disorders such as carbitis and ulcerative colitis; acadiovascular disorders such as createrial, fungal and parasitic infections diseases such as viral, bacterial, fungal and parasitic infections may also be treated using the proteins and polymucleotides of the invention. Sequences AAC95512 - CC AAC95520 and AAB52011 are used in the isolation and characterisation of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                       Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the proteins and polynucleotides of the invention
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                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                         Ruben SM, Komatsoulis G;
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Gaps

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GCCTGGGTTCCATGCCCCAGCTGTGGCCCCTCGTTCCCGAAGAGGGCTCGAGAC 480
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                                DB 8; Length 1036;
   Sequence 1036 BP; 368 A; 238 C; 235 G; 192 T; 0 U; 3 Other;
                                Score 385.6; DB 8; Length
Pred. No. 7.9e-92;
0; Mismatches 59; Indels
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12-SEP-2001; 2001US-00950082.
12-SEP-2001; 2001US-00950083.
                              78.4%;
87.8%;
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12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              atherosclerosis; stroke; endocarditis; congestive heart failure; rheumatic heart disease; cardiomyopathy; haemorrhoids; varicose veins; migraine; thrombosis; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; renal disorder; proliferative disorder; gene;
                                                                                                                                                 522
               CTCAGCCGGGACCCCTGGACCCCAATGAGTGTGGTTACCAACCCCCAGGAGCACCCCT
                                                                          GGCCTGGGTTCCATGCCCAGCTCCAGCTGTGGCCCTCGTTCCCGAAAGAAGGGCTCGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human secreted polypeptide and nucleic acid molecules, useful f diagnosing, preventing, prognosticating or treating cardiovascular disorders (e.g. arrhythmia, atherosclerosis, cardiomyopathy, or
                                                                                                                                                                                                                                                                                                                                                                                               secreted protein; cardiovascular disorder; arrhythmia;
                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein cDNA sequence #152
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12-SEP-2001; 2001US-00950082.
12-SEP-2001; 2001US-00950083.
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disorder;

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The invention comprises the amino acid and coding sequences of human secreted proteins. The DNA and protein sequences of the invention are useful for detecting, preventing, diagnosting, prognosticating, treating or ameliorating; haematopoietic or haematological disorders (e.g. anaemia and haemophilia); inflammatory disorders (e.g. inflammatory bowel disease wound healing and disorders of epithelial call proliferation; immune disorders of epithelial call proliferation; immune disorders (e.g. autoimmune disorders and asthmatic disorders); ardiovascular disorders (e.g. atherosclerosis and myocarditis); and gastrointestinal disorders (e.g. duodenal ulcers and gastrointestinal disorders (e.g. duodenal ulcers and gastroenteritis). The present DNA sequence encodes a human secreted protein of the invention.
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     gene therapy; human; secreted protein; haemopoietic disorder; haematological disorder; anaemia; haemophilia; inflammatory disordinflammatory bowel disease; Crohn's disease; neoplastic disease; leukaemia; wound healing; epithelial cell proliferation disorder; immune disorder; autoimmune disorder, asthmatic disorder; cardiovascular disorder; atherosclerosis; myocarditis; infectious disease; HIV; AIDS; endocrine disorder; diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10; Length 1036;
                                                                                                                              gastrointestinal disorder; duodenal ulcer; gastroenteritis;
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Pred. No. 7.9e-92;
); Mismatches 59
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12-SEP-2001; 2001US-00950082.
12-SEP-2001; 2001US-00950083.
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                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
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87.8%;
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Matches 432, Conservative
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                                                                                                                                                                    The invention relates to novel genes and their fragments which are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids and proteins are useful in the diagnosis, treatment and prevention of conditions are lated to diabetes, e.g. hyperglycaemia, obesity, retinopathy, polyneuropathy, atherosclerosis, anaemia, stroke, gangrene, impotence, infection, cataract, renal disorders, or endocrine disorders. The present sequence was used to illustrate the invention.
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                                                  A human secreted protein and nucleic acids useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating diabetes or conditions related to diabetes, e.g. hyperglycemia, obesity, retinopathy, neuropathy.
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                                                                                                                                                                                                                                                                                                                                                                                      Score 385.6; DB 8
Pred. No. 7.9e-92;
0; Mismatches 59
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                                                                                                                                     Claim 7; SEQ ID NO 132; 701pp; English.
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                  therapy, for identifying individuals from minute biological samples, as additional DNA markers for restriction fragment length polymorphism (RFLP), in forensic biology, molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response. The present sequence represents a human secreted protein encoding sequence of the
useful for chromosome identification, radiation hybrid mapping, in gene
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                                                                                                                                                                                                                                                                                               Score 385.6; DB 10; Length 1036;
Pred. No. 7.9e-92;
0; Mismatches 59; Indels 1:
                                                                                                                                                                                                                                                          Seguence 1036 BP; 368 A; 238 C; 235 G; 192 T; 0 U; 3 Other;
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Matches 432; Conservative
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                                                                                                                                                                                                            invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HGEDM64; HBHAA05; HBJCR46; HBJKD16; HCMSX51; HCQBH72; HDPPQ30; HE2CM39; HE9EA10; HGBHPD1; HLDQU79; Cytostatic; Hepatotropic; Antidiabetic; Antiinfanmatory; neuroprotective; Anti-HIV; Vulnerary; Gynecological; Antiinfertility; Gene therapy; gastrointestinal disorder; cancer; Alzheimer's disease; chromosome identification; ds.
                                                                                                                                                                                                                                    GGCCTGGGTTCCATGCCCAGCTCCAGCTGTGGCCCTCGTTCCCGAAGAAGGGCTCGAGAC
                                                                                                                                                                                                                                                               CTCAGCCGGGACCCCTGGACCCCAATGAGTGTGGTTACCAACCCCCAGGAGCACCCCT
                                                                                                                                                         CTCAGCCGGGACCCCTTGGACCCCCAATGAGTGTGGCTACCAGCCTCCAGGAGCACCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein encoding sequence #83.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; SEQ ID NO 93; 855pp; English.
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12-SEP-2001; 2001US-00950082.
12-SEP-2001; 2001US-00950083.
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The invention relates to an isolated polynuclectide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH5081, whose sequence was determined by the technique of SBH dequencing by Pybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for information of the novel polynucleotide. The nucleic acid sequences in forensics, in assessing biodiversities, or in identifying mutations in forensics, in assessing biodiversities, or in identifying mutations in forensics, in generating antisense DNA or RNA. The prefection of correction of the useful for generating antisense DNA or RNA. The prefect is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data of for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence than 1700-110-20030073623
                                                                                                                                                                                                        * polynucleotide sequences obtained from various cDNA libraries, useful
hybridization probes, as oligomers for PCR, for chromosome and gene
pping, in the recombinant production of protein, or in generating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                             Jones LW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 469 BP; 93 A; 141 C; 149 G; 86 T; 0 U; 0 Other;
                                                                                                                                           Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 76.0%; Score 373.8; DB 9 Local Similarity 99.2%; Pred. No. 8.5e-89; Nes 386; Conservative 0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 21099; 44pp; English.
                                                                                                                                         Stache-Crain B,
30-JUL-2001; 2001US-00918995
                                                               STACHE-CRAIN E
DICKSON M C.
JONES L W.
                                                                                                                                         Labat I,
                                  DRMANAC R T.
                                                                                                                                                                                                                                                               antisense DNA or RNA
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                                                    LABAT I
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                                                  (LABA/) 1
(STAC/) (
(DICK/) 1
(JONE/)
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                                  DRMA/)
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88; differential expression; colon cancer; cancer; human

11-OCT-2001; 2001US-00981353 11-OCT-2000; 2000US-0239841P.

US2002160382-A1

31-OCT-2002.

Human cDNA differentially expressed in colon cancer #1.

(first entry)

06-NOV-2003

ADA11077;

BP

ADA11077 standard; cDNA; 1168

combination comprising cDNAs that are differentially expressed in disorder, useful for diagnosing, treating, staging or monitoring

colon disorder, useful for d treatment for colon cancers.

Jones DA;

Lasek AW,

(LASE/) LASEK A W. (JONE/) JONES D A.

WPI; 2003-265756/26.

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The invention relates to a combination comprising cDNAs that are differentially expressed in colon disorder. The methods and compositions of the present invention are useful for disgnosing, treating, staging or monitoring treatment for colon cancer. They are also useful in high throughput methods for using cDNAs to detect differential expression of nucleic acids in a sample, screening molecules or compounds to identify a ligand which specifically binds a cDNA, and using a protein to screen molecules or compounds to identify at least one ligand which specifically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCTGGGTTCCATGCCCAGCTCCAGCTGTGGCCCTCGTTCCCGAAGAAGAGGCCTCGAGACAC 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                binds the protein. The present sequence represents a human cDNA differentially expressed in colon cancer.
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                                                                                                                                                                                                                                                                                                                                                                                  Score 368.4; DB 9; Length 1168; Pred. No. 2.8e-87;
                                                                                                                                                                                                                                                                                                                                Sequence 1168 BP; 249 A; 346 C; 339 G; 234 T; 0.U; 0 Other;
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Claim 1; SEQ ID NO 1; 231pp; English.
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182 812 242 752 302

692 362 632 422 572

> GCTCAGCCGGGACCCCTGGACCCCAATG 388

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This invention relates to novel isolated cDNAs that are differentially expressed in MYCN activated cells. Specifically, it refers to polynucleotide sequences that exhibit differential expression patterns in cells activated by the transactivator MYCN, where MYCN is a protononcogene that is amplified in neuroblastoma cells and is common in small cell lung cancers. The present invention describes these cDNA molecules as useful for in hybridisation assays to detect expression of nucleic acids (or complementary nucleic acids) in a present in a given sample, well as for screening assays by identifying molecules or compounds that specifically bind the cDNA as a ligand and modulate function or activity. Accordingly, these compositions exhibit cytostatic activity and can also be used for gene therapy purposes. This polynucleotide sequence is a cDNA that is differentially expressed in MYCN activated cells, given in an the printed specification but has been obtained in electronic format from the US Patent Office at
CCTGGGTTCCATGCCCAGCTCCAGCTGTGGCCCTCGTTCCCGAAGAGAGCTCGAGAAAC 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New genes regulated by MYCN activation, useful in gene therapy, particularly for treating a subject with e.g. neuroblastoma or other cancers, or for diagnosing, staging or monitoring the treatment of the
                                                                                                                                                                                                                                                                                                                                               88;
                                                                                                                                                                                                                                                                                    Human cDNA differentially expressed in MYCN activated cells SegID
                                                                                                                                                                                                                                                                                                                   human; differential expression; transactivator; proto-oncogene; neuroblastoma; small cell lung cancer; cytostatic; gene therapy; MYCN activated cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1168 BP; 249 A; 346 C; 339 G; 234 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.seqdata.uspto.gov/sequence.html?DocID=20030119009.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shohet JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 60; 27pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plon SE,
                                                                                                                                                                                 ADJ56254 standard; cDNA; 1168 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-2002; 2002US-00084817.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-FEB-2001; 2001US-0270784P
                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nuchtern JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (STUA/) STUART S G.
(NUCH/) NUCHTERN J G.
(PLON/) PLON S E.
(SHOH/) SHOHET J M.
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                                                                                       CCGATCGTGA
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                                                                                                        GCACCAGCTCACCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACC 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
                                                               GCACCAGCTCACCAAGCTACGTTTCCTTCAAGACTGAAGACAGCTGGGTCCCAGCCTCACC
                                                                                                                                                                                     CAGCCGGGACCCCCTGGACCCCCAATGAGTGTGGTTACCAACCCCCCAGGAGCACCCCCTGG
                                                                                                                                                                                                                                                                                            CCTGGGTTCCATGCCCAGCTCCAGCTGGCCCCTCGTTCCCGAAGAAGGGCTCGAGACAC
                                                                                                                                                                    TGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTGCTGCT
                                                                                                                                                                                                                                CAGCCGGGACCCCCTGGACCCCAATGAGTGTGGGTTACCAACCCCCAGGAGCACCCCTGG
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                                               CAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGGTCCCAGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 3603; 71pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted protein 5' EST, SEQ ID NO: 3603.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC03605 standard; cDNA; 303 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-FEB-2000; 2000EP-00200610.
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                                                                                                                                                                                                                                                                                                                                                                      CCGATCGTGA 492
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74.9%; Score 368.4; DB 10; Length 1168; 99.7%; Pred. No. 2.8e-87; o) Mismatches 1; Indels 0;

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Gaps

Matches 369; Conservative

Similarity

Query Match Best Local S

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mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                 68 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 127
                                                                                                                                                                                                                                                                                                                                                                                                 121 GGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGGCTCTCGGCATGTAGTGTTCTCAGGTTCT 180
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48.0%; Score 236; DB 3; Length 303;
Best Local Similarity 100.0%; Pred. No. 1.8e-52;
Matches 236; Conservative 0; Mismatches 0; Indels
                                                                                                                      Sequence 303 BP; 57 A; 81 C; 105 G; 60 T; 0 U; 0 Other;
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Search completed: January 31, 2005, 16:45:02 Job time : 395 secs

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RESULT 1
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 Sequence 459, App
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Sequence 237341,
Sequence 237821,
Sequence 225595,
Sequence 308929,
Sequence 60670, A
Sequence 61107, A
Sequence 61107, A
Sequence 61107, A
                                                                                    January 26, 2005, 15:06:38; Search time 135.925 Seconds (without alignments) 433.254 Million cell updates/sec
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861
1 MEHYRKAGSVELPAPSPMPQ......SMPSSSCGPRSRRRARDTRS 163
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Compugen Ltd.
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US-10-425-115-308955
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Sequence 459, Application US/09731872

Sequence 459, Application US/09731872

Sequence 459, Application US/09731872

Sequence 459, Application US/09731872

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dumas Milne Edwards, Jean

APPLICANT: Dumas Milne Edwards, Jean

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78.US3.REG

CURRENT APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR APPLICATION NUMBER: US 60/187,470

NUMBER OF SEC ID NOS: 482

SOFTWARE: Patent.pm

SEC ID NO 459

LENGTH 1.174
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Sequence 201476, Sequence 201476, A
Sequence 125743, Sequence 121222, Sequence 119229, A
Sequence 134549, Sequence 134549, Sequence 266917, Sequence 266917, Sequence 201766, Sequence 201766, Sequence 224520, Sequence 224520, Sequence 120639, Sequence 12144, Ap Sequence 11365, Ap Sequence 226639, Sequence 11365, Ap Sequence 226639, Sequence 11365, Ap Sequence 226639, Sequence 11365, Ap Sequence 236639, Sequence 236639, Sequence 11365, Ap Sequence 2464, A
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Sequence 109378,
Sequence 156973,
Sequence 191078,
Sequence 45240, A
Sequence 60641, A
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US-10-437-963-156973

US-10-437-963-156973

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US-10-425-115-308917

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US-10-425-115-308917

US-10-425-115-308917

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US-10-425-115-26917

US-10-425-115-26917

US-10-425-115-26917

US-10-425-115-26917

US-10-425-115-278508

US-10-437-963-181400

US-10-437-963-181400

US-10-437-963-181400

US-10-437-963-181400
ORGANISM: Homo sapiens
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Sequence 237441, Application US/10425115
Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
APPLICANT: Las Cosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With FILLE OF INVENTION: Plants
FILE REPRENCE: 38-21(5322)8
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
SEQ ID NO 237341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
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  PRIOR FILING DATE: -09-04

PRIOR FILING DATE: -09-04

PRIOR PELING DATE: 1998-11-13

PRIOR PILING DATE: 1998-11-13

PRIOR FILING DATE: 1998-12-17

PRIOR FILING DATE: 1998-12-17

PRIOR PILING DATE: 1998-12-17

PRIOR FILING DATE: 1999-02-09

PRIOR FILING DATE: 1999-02-09

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 810

SOFTWARE: Patent.pm

LENGTH: 163
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94.4%; Score 813; DB 11; Length 163;
Best Local Similarity 94.5%; Pred. No. 5.3e-72;
Matches 154; Conservative 1; Mismatches 8; Indels
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US-10-425-115-237341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70, 103, 107, 108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature
; LOCATION: (36, 47, 54, 65,
; OTHER INFORMATION: unknown
US-09-978-360A-668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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Matches 62; Conserv
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ORGANISM: Zea mays
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                                                                                                                                                            Sequence 459, Application US/09876997

Publication No. US20030152921A1

Publication No. US20030152921A1

Publication No. US20030152921A1

APPLICANT NORMATION:

APPLICANT: Bougueleret, Lydie

APPLICANT: Jobert, Severin

TILE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.104.CIP

CURRENT APPLICATION NUMBER: US/09/876,997

CURRENT PILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 60/181,470

PRIOR APPLICATION NUMBER: US 60/189,629

PRIOR FILING DATE: 2000-03-06

PRIOR FILING DATE: 1999-12-08

NUMBER OF SEQ ID NOS: 482

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Sequence 668, Application US/09978360A

Publication No. USZ0040110939A1

GENERAL INFORMATION:

APPLICANT: Edwards, Jean-Baptiste Dumas Milne

APPLICANT: Bougueleret, Lydie

APPLICANT: Glueel, Catherine

APPLICANT: Clusel, Catherine

TITLE OF INVENTION: Complementary DNA'S Encoding Proteins with Signal Peptides

FILE REFERENCE: 56.US4.CIP

CURRENT APPLICATION NUMBER: US/09/978,360A

CURRENT FILING DATE: 1997-11-13

PRIOR PILING DATE: 1997-12-17

PRIOR FILING DATE: 1997-12-17

PRIOR FILING DATE: 1998-02-09

PRIOR FILING DATE: 1998-04-13

PRIOR FILING DATE: 1998-08-10

PRIOR FILING DATE: 1998-08-10

PRIOR FILING DATE: 1998-08-10

PRIOR FILING DATE: 1998-08-10

PRIOR FILING DATE: 1998-08-10
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Pred. No. 9.7e-77;
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100.0%;
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Best Local Similarity 100.
Matches 163; Conservative
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US-09-876-997-459
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LENGTH: 163
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Squence 229595, Application US/10424599

Fublication No. US20040031072A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Vongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules
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TITLE OF INVENTION:
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Fublication No. US20040214272A1
Fublication No. US20040214272A1
Fublication No. US20040214272A1
Fublication No. US20040214272A1
FublicANT: La Rosa, Thomas J.
APPLICANT: Cavalic, David K.
APPLICANT: Cav, Yongwal
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPRENCE: 38-21(5322)B
FUBLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 308895
LENGTH: 276
                                                                                                                                                                                                                                                                                    61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
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                                                                                                                                      1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS 60
                                                                                                                                                                                                           1 MDRYOR-----VEKPRNETPIRENEIRITALGRMRNYIGYGMSLLEENGHDEITIKAM 53
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LSKKELDISSTGYQPP-LPVDQVKPLNEYDEEGEGS-----PRIRGRGR 154
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Pred. No. 1e-13;
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US-10-424-599-229595
                                                                 23; Mismatches
                              33.1%;
                                                             57; Conservative
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ORGANISM: Glycine max
                       Best Local Similarity
Matches 57; Conserv
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
ITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
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Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
RAPPLICANT: La Rosa, Thomas J.
APPLICANT: Cavalic, David K.
APPLICANT: Cao, Youna
APPLICANT: Cao, Youna
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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26.4%; Score 227; DB 15; Length 281;
Best Local Similarity 31.8%; Pred. No. 6.2e-14;
Matches 56; Conservative 24; Mismatches 66; Indels 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.0%; Score 224; DB 17; Length 242;
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US-10-424-599-237821
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OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                             Sequence 237821, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                       GRAAGKAVSCAE 72
                                                                                    61 GRAARNAVSFAE 72
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ORGANISM: Glycine max
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ORGANISM: Zea mays
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; OTHER INFORMATION: Clone ID: LIB3357-033-B9_FLI.pep
US-10-425-114-60670
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; OTHER INFORMATION: Clone ID: LIB3332-020-F9_FLI.pep
US-10-425-114-61107
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114 LSKNPLDTSSPGYQPP 129
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137 LSKNPLDTSSPGYQPP 152
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Best Local Similarity
Matches 46; Conserv
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                                                                                                                                   SEQ ID NO 60670
LENGTH: 278
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Bublication No. US20040214272A1
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Enou, Yinua
APPLICANT: Application Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 308929
                                                                                                                                                                                                                                                                            61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
                                                                                                                                                                                                                                                                                                         61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
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                                                                                                            DB 17; Length 276;
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23.6%; Score 203.5; DB 17; Length 276;
Best Local Similarity 33.8%; Pred. No. 1.3e-11;
Matches 46; Conservative 19; Mismatches 62; Indels 9;
                                                                                                                                                       Indels
                                                                                                      Query Match 23.6%; Score 203.5; DB 17; Best Local Similarity 33.8%; Pred. No. 1.3e-11; Matches 46; Conservative 19; Mismatches 62;
                                   ) OTHER INFORMATION: Clone ID: MRT4577_4477C.1.pep
US-10-425-115-308895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; CTHER INFORMATION: Clone ID: MRT4577_4480C.1.pep
US-10-425-115-308929
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Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Rovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                               121 LSRDPLDPNECGYOPP 136
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112 LSKNPLDTSSPGYQPP 127
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112 LSKNPLDTSSPGYQPP 127
ORGANISM: Zea mays
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Sequence 61107, Application US/10425114

Sequence 61107, Application US/10425114

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Enou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: GF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement TITLE REFERENCE: 38-21(53313) B
CURRENT PELING DATE: 2003-04-28
NUMBER OF SEO ID NOS: 73128
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Wolcleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION WUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GRAAGKAVSCAEIVKRRVPGLHQLIKLRFLQTEDSWVPASPDIGLDPLTVRRHVPAVWVL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
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Sequence 60913, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)8
CURRENT APPLICANT: 2003-04-28
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
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Fublication No. US2004021427241
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5122)B
CURRENT PELIGO DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 232929
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                                                                                                             103 GRAINKTVMVVELIKRRVGGLHQNTATESVDITDTWEPL--EEGLLPLETTRHVSMITVT 160
                                                                              61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
40 MDRYQR-----VEKPRNDTPISQNEIRITTQGRMRNYISYGMSLLEENGHDEISIKAM 92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 325;
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US-10-425-114-60913
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151 LSKNPLDTSSPGYQPP 166
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161 LSKNPLDTSSPGYQPP 176
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Zea mays
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ORGANISM: Zea mays
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Sequence 58679, Application US/10425114

Sequence 58679, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska: Jack E

APPLICANT: Tabaska: Jack E

APPLICANT: Title OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                        APPLICANT: Zhou, Yimuma APPLICANT: Zhou, Yimuma APPLICANT: Zhou, Yimuma APPLICANT: Screen, Steven E APPLICANT: Tabaska, Jack E APPLICANT: Tabaska, Jack E APPLICANT: Cao, Yongwei TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313) ECURRENT APPLICATION NUMBER: US/10/425,114
CURRENT PILING DATE: 2003-04-28
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OTHER INFORMATION: Clone ID: UC-ZMFLMO17184G05_FLI.pep
US-10-425-114-54515
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US-10-425-114-58679
                                          US-10-425-114-54515; Application US/10425114; Sequence 54515, Application US/10425114; Publication No. US20040034888A1; GENERAL INFORMATION: APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 LSRDPLDPNECGYQPP 136
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151 LSKNPLDTSSPGYOPP 166
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Best Local Similarity 33.8%
Matches 46; Conservative
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Best Local Similarity 33.8*
Matches 46; Conservative
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; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_144024C.1.pep
US-10-425-115-232929
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	Gaps	IVVESGS	: IVIKAM	PAVWVL	SLITIK	AR 159	GR 163
78;	30;	GGSARE	: DNATDI	IVRRH	STIRHA	PRSRRE	ARSRGE
Length 1.	Indels	GLĄĻGRĻE	TYALALLQI	PDTGLDPL	- EEGLVTL	SMPSSSCGI	RGRGI
17;	, 70;	KIRNLI	: : RPRNYI	SWVPAS	: rwepl-	рреде	 VPSGRG
23.5%; Score 202; DB 17; Length 178; 30.1%; Pred No 1e-11;	fismatches	TLEMRVRDGS	: : SANEIRITAQG	TKLRFLQTED	: : TSIESIDITD	5	PADFDQDAEA
.5%; Scor	e 23; N	Idd TÖdWd Sd	EKPREESPIC	KRRVPGLHOI	: KRRIAGLHON	PP	 PPIPADQVRE
Query Match 23.5%; Score 202; DB 17 Best Local Similarity 30.1%; Pred No 1e-11.	Matches 53; Conservative 23; Mismatches 70; Indels 30; Gaps	1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLIGLALGRLEGGSARHVVFSGS 60		61 GRĄAGKAVSCAEIVKRRVPGLHQLĮKLRFLQTEDSWVPASPDIGLDPLIVRRHVPAVWVL 120	54 GRAINKTVAIVELLKRRIAGLHQNTSIESIDITDTWEPLEEGLVTLETIRHVSLITK 111	121 LSRDPLDPNECGYOPPGAPPGLGSMPSSSCGPRSRRRAR 159	
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Search completed: January 26, 2005, 15:28:35 Job time: 136.925 secs

Mus

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Run on:

Sequence:

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Ranmania butneria; Firmates; Catarinii; Hominiade; Homo.

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausmer, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Alschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Morce, T., Wax, S.I., Wang, J., Haish, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M., B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Uddin, T.B., Toshiyuki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abrameon, R.D., Mullah, S.J., Bosak, S.A., McEwant, P.J.,

Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Vilalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Butterfield, Y.S., Krzywinski, M.I., Schlska, U., Shavchenko, Y.,

Butterfield, Y.S., Krzywinski, M.I., Shalska, U., Smailus, D.E.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

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                        CQ735345 Sequence
AY034074 Homo sapi
BC002497 Homo sapi
BC002497 Homo sapi
AR447527 Sequence
AR447527 Sequence
AR447527 Sequence
AR429315 Homo sapi
BX931336 Gallus ga
AF429315 Homo sapi
BX94615 Gallus ga
AC023362 Mus muscu
BT011363 Drosophil
Continuation (14 o
CQ592263 Sequence
AK655393 Sequence
AK073476 Homo sapi
AC071811 Homo sapi
AC0718128 Rattus no
AC118128 Rattus no
AC118128 Rattus no
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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BT011363
BT011363
CQ592263
AX655393
AY089619
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AR447527
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AK000381
BX931336
AF429315
AC107974
BX934615
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AE017228
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KEYWORDS
SOURCE
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REFERENCE
AUTHORS
TITLE
JOURNAL
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AL160270 Human DNA
BD139494 Extended
AR412580 Sequence
AX669414 Sequence
BD108133 EST and e
AC098197 Rattus no
AC110351 Rattus no
AC33897 Mus muscu
BC047068 Mus muscu
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AX887740 Sequence
BD027350 Sequence
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AC095805 R
AC108546 R
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Copyright (c) 1993 - 2005
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88

Minimum I Maximum I

Database

Result 80.

us-10-057-813-13.rge

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Direct Submission

AL Charlest Submission

Submitted (27-APR-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 18A, UK. Email anquirtes: humquery@sanger.ac.uk Clone
requests: clonerequesc@sanger.ac.uk

On Mar 24, 2001 this sequence version replaced gi:13274314.

During sequence assembly data is comparated as variations

Uning sequence asce found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em; EMBL; Sw;
SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
httn://www.earcas.arcas.ur/const.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.arcas.ar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
                                                                                                                                                                                                                                                                                                                                                                                                                                      RP11-296L22 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence is the entire insert of clone RP11-296L22 The true left end of clone RP11-443P11 is at 176963 in this sequence. The true right end of clone RP11-573M23 is at 15950 in this sequence. Location/Qualifiers
                                                      CTGCACCAGCTCCCCAAGCTATCCTTCAGACTGAGGACAGCTGGGTCCCCAGCCTCA
                                                                                                                                                                                                            CCTGACACAGGGCTAGACCCCCTCACAGTGCGCCCCATGTGCCTGCAGTGTGGGTGCTG
                                                                                                                                                                                                                                                                                                   CTCAGCCGGGACCCCCTGGACCCCCAATGAGTGTGGTTACCAACCCCCAGGAGCACCCCT
                                                                                                                                                            CCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGGGTGCTG
                     CTGCACCAGCTCCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCA
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AL160270/c
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                                                                                                                                                                                                                                                                                                              Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Neb site: http://www.nisc.nih.gov/
Akhter.N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakeeley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakeeley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Hansen,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Madurco,Q.L., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McClowell,J., Peargeon,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 39 Row: h Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22325369. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein id="AAH32136.1"
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TGLDPLTVRRHVPAVWULLSRDPLDPNECGYQPPGAPPGLGSMPSSSCGPRSRRRARD
TRS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGGAGCACTACCGGAAAGCTGGTCTGTAGAGCTCCCAAGCGCCCTTCCCCAATGCCCCAG 60
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                                                                                                                                                                               CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
NIH-MGC Project URL: http://mgc.nci.nih.gov
On Aug 19, 2003 this sequence version replaced gi:21618954.
Contact: MGC help desk
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/db_xref="LocusID:138716"
                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
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Matches 492; Conserv
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/db xref="taxon:9606" /chromosome="9" 200.000	- Copies / 1 met 83\$ - 1402 - AluSx repeat: matche 1644 - 1709 - 1709 - 1999 - 1999 - 11999 - 11999 - 11999 - 11999 - 11999 - 11999 - 11999 - 11999	1312 of consensu 61316183 of cons 1276 of consensu- nnserved" 18 conserved" 10109 of consensus 3257 of consensus 342693 of consensus	/note="AluJb repeat: matches 1305 of consensus" 78308610 70208610 86898789 7040	1490415540 Inote="FLAM C repeat: matches 5141 of consensus" 150481519 Inote="AluY repeat: matches 40311 of consensus" 15171552 Inote="AluD repeat: matches 118310 of consensus" 1601016045 Inote="Stand A repeat: matches 118310 of consensus" Inote="PLAM A repeat: matches 1132 of consensus" Inote="FLAM A repeat: matches 2160 of consensus" Inote="MIR repeat: matches 2160 of consensus" Inote="Liz repeat: matches 12731754 of consensus" Inote="Liz repeat: matches 11126 of consensus" Inote="Liz repeat: matches 68677071 of consensus" Inote="Liz repeat: matches 20132338 of consensus"

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Edwards,J.-B.D.M., Jobert,S. and Giordano,J.-Y.
EST's and encoded human proteins
Patent: US 6639063-A 217 28-OCT-2003;
Location/Qualifiers
                                                                                                                                                                                                                    Query Match 98.4%; Score 484; DB 6; L
Best Local Similarity 97.8%; Pred. No. 1.6e-112;
Matches 481; Conservative 8; Mismatches 3;
                                   Location/Qualifiers
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Sequence 217 from patent US 6639063.
                                                                                                                            1. .884
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69. .224
849. .854
870. .883.
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score 4.69999980926514
seq LGLALGRLEGGSA/RH
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polyA_signal
polyA_site
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PN JP 2002508182-A/246
PD 19-MAR-2002
PD 19-MAR-2003
PF 17-DEC-1997 US 60/069957,09-FEB-1998 US 60/074121 PR
13-APR-1998 US 60/091563,10-AUG-1998 US 60/096116 PI LYDIE
BOUGUELERET,AYMERIC DUCLERT,JEAN BAPTISTE DUMAS MILNE PI EDWARDS
PC CIIZNIS/09,CIZNIS/09,CO7K14/47,CO7K16/18,CIZNI/15,CIZNI/19, PC
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PC C12N5/10,C12P21/02,C12Q1/68,C12N15/00,C12N5/00,C12N15/00 CC
Von Heijne matrix
45795. .45925
/norbe="AluSq repeat: matches 5. .135 of consensus"
45953. .46118.
/note="LIME2 repeat: matches 5933. .6155 of consensus"
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Pred. No. 8.6e-115;
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                                                                        Query Match
100.0%; Score 492; D)
Best Local Similarity 100.0%; Pred. No. 8.6
Matches 492; Conservative 0; Mismatches
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BD139494
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JP 2002508182-A/246.
Homo sapiens (human)
Homo sapiens
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195468 ACCCGATCGTGA 195457
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PAT 18-SEP-2002
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                               CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG 120
                                                                                                                            CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG 197
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C12N1/21,
C C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC C12N15/00
C VON Heijne matrix
CC Score 4.6999980926514
CC Seq LGLALGRLEGGSA/RH
FY CDS TO C TOCATION Qualifiers
FT CDS TO C TOCATION TO
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Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.
ExT and encoded human protein
Patent: JP 2002010789-A 210 15-JAN-2002;
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PD 15-2020100189-A/210
PD 15-3AN-2002
PF 07-AUG-2000 JP 2000280989
PR 05-AUG-1999 US 60/147499
PI JEAN BAPUTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE GIORDANO
                                                                                                                                                                                                                  198 GGGTTGGCTCTGGGTCGGTTGGAGGCGGCAGTGCTCCGGCATGTAGTGTTCTCAGGTTCT
       1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCCAATGCCCCAG
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76.1%; Score 374.4; DB 6; Length 461;
Best Local Similarity 98.4%; Pred. No. 1.3e-84;
Matches 376; Conservative 2; Mismatches 4; Indels 0
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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GRLEGGSARHVVFSGSGRAAGKAVSCARIVKRRVPGLHQLTKLRFLQTEDSWVPASPD
TGLDPLTVRRHVPAVWVLLSRXPWTQ"
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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76.1%; Score 374.4; DB 6; Length 461;
Best Local Similarity 98.4%; Pred. No. 1.3e-84;
Matches 376; Conservative 2; Mismatches 4; Indels 0
                                               Length 461;
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ESTs and encoded human proteins
Patent: EP 1104808-A 217 06-JUN-2001;
Genset (FR)
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db_xref="taxon:9606"
78. _>461
/note="unnamed protein product"
/codon start=1
/protein.id="CAF14522.1"
/db_xref="G1:40975748"
                                               DB 6;
                                             76.1%; Score 374.4; DB 6 98.4%; Pred. No. 1.3e-84; iive 2; Mismatches 4
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Sequence 217 from Patent EP1104808.
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Homo sapiens
                                             Query Match 76.1
Best Local Similarity 98.4
Matches 376; Conservative
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Muzny, D. Marte., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, H., Algbrooks, S., Amin, A., Anguiano, D., Allen, H., Algbrooks, S., Amin, A., Anguiano, D., Allen, H., Algbrooks, S., Amin, A., Anguiano, D., Banderchi, W., Baca, B., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Burch, P., Burch, P., Burrell, K., Caleron, E., Cardenas, V., Chavez, D., Chen, G., Chen, Y., Center, A., Chavez, D., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J., Cardenas, V., Carter, K., Coxirell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Daraper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Foster, M., Garza, M., Gebregoorgis, E., Geer, K., Gali, R., Garday, M., Guerra, W., Guerra, W., Gabisi, A., Ganea, R., Henderson, N., Hernandez, S., Haaland, C., Callis, R., Haaland, C., Callis, R., Hawes, A., Handlico, C., Hamilton, C., Hamilton, K., Hollins, B., Howells, S., Hladun, S.L., Hodgson, A., Hogues, M., Jackson, L., Jacobb, L., Jang, H., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Lorensuhewa, L., Loulseged, H., Loadon, P., Lowis, L., Lu, X., Malling, S., McLeod, M.P., Martin, R., Martinez, E., Mawhiney, S., McLeod, M.P., Martin, R., Martinez, E., Mandiney, S., Morleod, M.P., Mortel, R., Mortensy, M., Morris, K., Morris, S., Morleod, M., Minja, E., Montenney, R., Morris, S., Morleod, M., Minja, E., Montensy, Mullosavijevic, A., Morris, S., Morleod, M.P., Morris, S., Morleod, M.P., Morris, S., Morleod, M.P., Morris, S., Morleod, M. Minja, E., Morlensy, M., Morris, S., Morleod, M. Morris, S., Morley, M., Morris, S., Morley, S., Morley, S., Morley, S., Morle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCUSELY 238811 bp DNA linear HTG 13-MAY-2003 Rattus norvegicus clone CH230-9714, WORKING DRAFT SEQUENCE, 10 unordered pieces.
                           137
                                                                                                                                                          197
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
18 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG
                                                                                                                           CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAATTCGCAACCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                         CTGCACCAGCTCACCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGGTCCCAGCCTCA
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                                                                                         CTACCTCCTGATACCCTTGAGATGCGGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG
                                                                                                                                                                                                                        121 GGGTTGGCTCTGGGTTGGAGGGCGGCAGTGCTCGGCAJGTAGTAGTGTTCTCAGGTTCT
                                                                                                                                                                                                                                                                                                                                                       GGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTCCCAGGC
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
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KEYWORDS
SOURCE
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Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 13, 2003 this sequence version replaced gi:24819301.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/ratl/): Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwackelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Perez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L. L.,
Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,
Reilly, M., Relly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., Shen, H.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Sneeth, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Steinle, M., Strong, R., Sitton, A., Svatek, A., Tabor, P., Taylor, T.
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Veray, V., Villaenan, D., Walker, B., Wander, S., Warren, J., Warren, C., Wang, C., Warren, C., Warren, C., Warren, C., Warren, C., Wang, C., Warren, C., Warren, C., Wang, C., Warren, C., War
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Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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44755: contig of 44755 bp in length

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SE MARTOLD. MARIEL. MEZEKAN. LEEL. ADREMEZON, S., Addame, C., Alder, J.,
Allen, C., Allen, H., Alsbrooke, S., Adnin, A., Angulano, D.,
Allen, C., Allen, H., Alsbrooke, S., Adnin, A., Angulano, D.,
Bandarie, Mezker, M., Ayodeji, M., Bacar, B., Badeh, H.,
Baldyalbok, R., Blair, J., Blankenburg, K., Bilyh, P., Brown, M.,
Bandwalo, M., Blair, J., Blankenburg, K., Bilyh, P., Brown, M.,
Bryant, M., Carter, K., Cavazos, I., Censar, H., Center, A.,
Chacko, J., Chave, D., Cheng, C., Chen, R., Chen, J., Chu, J.,
Cheveland, C., Caver, D., Cheng, C., Chen, M., Cree, M., Devert, D.,
Duggado, O., Denson, S., Davy, Cartoll, L., De And, C., Dederch, D.,
Duggado, O., Denson, S., Davy, Cartoll, L., De And, C., Dederch, D.,
Duggar, M., Enger, M., Engen, C., Devin, M., Duya, K.,
Egan, A., Bougar, Rocha, S., Dunn, M., Dutya, K.,
Duggar, R., Shiley, M., Flaggy, M., Guerer, M., Gevere, P.,
Fraesc, C.M., Gabisla, A., Galla, R., Garter, M., Guevara, W.,
Gunaratte, P., Havlak, P., Haves, A., Handleon, N., Hermadez, M.,
Hernandez, R., Hilles, S., Hladun, S. L., Hodgoon, A., Hogues, M.,
Hernandez, R., Hilles, S., Hulyk, S., Hamel, D., Dubson, R.,
Johnson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R.,
Johnson, L., Jacob, H., Liu, Y., London, P., Longac, F., Morgue, M.,
Mangum, B., Mapu, P., Martin, K., Martin, R., Martinez, E.,
Mayolu, Morris, K., Morris, S., Munden, S., Morgan, M., Morris, S.,
Morgan, M., Worris, S., Meled, M., Nortis, S.,
Morgan, M., Wortis, S., Munden, M., Nayer, P., Lu, C.,
Plopper, F., Poindexter, A., Perez, L., Fannkoch, C.,
Plopper, F., Poindexter, A., Svatch, A., Trabor, P., Wang, T.,
Mangum, S., Sabertern, S., Munden, M., Reber, R.,
Resilly, B., Reilly, M., Ren, S., Scott, G., Sher, M.,
Resilly, B., Reilly, M., Ren, S., Scott, G., Sher, M.,
Sardern, M., Strong, R., Stutcen, A., Svatck, A., Trabor, P., Weng, T.,
Mang, G., Walle, R., Wu, J., Yakb, S., Yen, J., Yoon, V.,
Walliame, G., Willaen, R., Weise, R.,
Mang, G., Waller, M., Weise, R.,
Mang, G., Waller, M., Weise, R.,
Mang, G., Waller, M., Weise,
                                                                                                                                                          AC110351 242324 bp DNA linear HTG 12-OCT-2002 Rattus norvegicus clone CH230-217H18, WORKING DRAFT SEQUENCE.
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Submitted (11-FEB-2002) Human Genome Sequencing Center, Department
Subjectiar and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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ACI10351.4 GI:23915435
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
              149574 ACCCGGTCCTGA 149563
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44855: gap of unknown length
129903: contig of 8548 bp in length
130003: gap of unknown length
227138: contig of 97135 bp in length
227238: gap of unknown length
229033: contig of 1745 bp in length
229035: contig of 1242 bp in length
230425: gap of unknown length
23444: contig of 2019 bp in length
23455: gap of unknown length
23455: contig of 2019 bp in length
23455: contig of 1711 bp in length
23455: gap of unknown length
23455: gap of unknown length
235510: contig of 1355 bp in length
235510: gap of unknown length
235620: contig of 1010 bp in length
236820: contig of 1010 bp in length
236820: contig of 1010 bp in length
236820: contig of 1891 bp in length
                                     of 85048 bp in length
unknown length
of 97135 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
/mol type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-9714"
3538. 4289
/note="clone boundary
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site:EcoRl
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44856. .46019
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128441. 129903
/note="wgs_contig"
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Best Local Similarity 84.8
Matches 417; Conservative
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228984
239984
239084
230326
2322445
2322445
234256
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2358111
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12828 GGCCGGGCCGCTGGAAAGGCCGTCAGCTGTGCAGATTGTCAAACGGCGGGTTCCGGGC 12769
                                                                                         13008 ATGGAGCACTACCGGAGGGCTGGCTCTGTAGAGCTCCCAGCCTCATCACCAATGCCCCAG 12949
                                                                                                                                                                              12948 CTACCTCCCGACACGCTGGAAATGCGGGTCCGAGATGGGAGCAAAATCCGAAACCTACTA 12889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12648 CTTAGTCGGGACCCCTTGGACCCCAGTGAATGTGGCTACCAACCCCCAGGTGCACCTCCT 12589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jevolella, C.
Direct Submission
Submitted (01-SEP-2000) Ievolella C., CRIBI Biotechnology
Centre-Compl. Interedipartim. Vallisneri, Universita' di Padova, via
Ugo Bassi 58/b, 35121, ITALY
Ugo Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         834 bp mRNA linear ROD 19-MAR-2001
Mus musculus mRNA for hypothetical protein (ORF1), related to clone
AJ293897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               levolella,C., Zara,I. and Lanfranchi,G.
Full length sequencing of some human and murine muscular transcript
(Telethon Italy project B41)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                      CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGCCAGCAAAATTCGCAACCTGCTG
                                                                                                                                                                                                                         GGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGGTGCTG
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|tissue_lib="Stratagene UnizAP XR vector"
        Indels
        75;
        Mismatches
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/db xref="taxon:10090"
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Mus musculus
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ORF1.
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        417; Conservative
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        Matches
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KEYWORDS
SOURCE
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                                                     Submitted (12-0CT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA
On Oct 12, 2002 this sequence version replaced gi:21739791.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.two.edu/projects/art/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by the finished sequence as soon as it is available and the accession number will be preserved.

1 242324: contig of 242324 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 372; DB 2;
Pred. No. 2.9e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="wgs_end_extension
clone_end:T7"
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/note="wgs_end_extension
clone_end:T7"
                      Genome Sequencing Consortium.
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note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="CH230-217H18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              boundary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="clone_br
clone_end:Sp6
site:EcoRI
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84.8%;
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site:EcoRI
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                                            Direct Submission
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Best Local Similarity
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                 AUTHORS
TITLE
JOURNAL
REFERENCE
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Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Hulyk, S.W., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakealey, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalbka, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 45 Row: b Column: 9 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MRQYRRAGSVELPASSPMPQLPPDTLEMRVRDGSKIRNLLGLAL
GRLEGGSTRHVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPTSPD
TGLDPLTVRRHVPAVWVLLSRDPLDPSECGYQPPGAPPGLGSIPSPSCGPRFRRRARD
TRS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web Site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,
A.N., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 month
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Straubberg, R.
Direct Submission
Submitted (19-FEB-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing Usy: Baylor College of Medicine Human Genome
Sequencing Center
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old mouse. Taken by biopsy."
/clone lib="NCI CGAP_Mam2"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/codon_start=1
product="RIKEN cDNA 2810432D09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N-3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="2810432D09Rik"
/db_xref="LocusID:69961"
/db_xref="MGI:1917211"
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|db_xref="GI:28436879"
|db_xref="LocusID:69961"
|db_xref="MGI:1917211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   human and mouse cDNA sequences
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related to clone Telethon(Italy_B41)_Strait02713_FL143"
/codon_start=1
/product."hypothetical_protein"
/protein_d="CAC34588.1"
/db_xref="df:12397925"
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GRIEGGSTRHVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRPLQTEDSWVPTSPD
TGLDPLTVRRHVPAVWYLLSRDPLDPSECGYQPPGAPPGLGSIPSPSCGPRPRRRARD
TRS"
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Mus musculus RIKEN cDNA 2810432D09 gene, mRNA (cDNA clone MGC:32232 MGCE:5009034), complete cds.
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Straubserg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klauener, R.D., Collins, F.S., Wagner, L., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 CTACCTCCTGACACTCTGGAATGCGAGTCCGAGATGGGAGCAAAATCCGAAACCTGCTA 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 370.4; DB 10;
Pred. No. 1.3e-83;
); Mismatches 76;
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BC047068.1 GI:28436878
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Best Local Similarity 84.6%;
Matches 416; Conservative C
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B Harrison, E. Direct Submission

Direct Submission

Loud (10-FBE-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBlO 158, UK. E-mail enquiries:

Numquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Jan 30, 2003 this sequence version replaced g1:2755583.

Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
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Mouse DNA sequence from clone RP23-167112 on chromosome 4, complete
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0
                                                            Score 370.4; DB 10; Length 863; Pred. No. 1.3e-83; 0; Mismatches 76; Indels 0;
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Contact: humquery@sanger.ac.uk
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84.6%;
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ORIGIN
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Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMEL; Sw., SWISSENCT; Tr., TERMBL; Wp., WORWPEP; Information on the WORMPEP database can be found at the world stable search be found at the world stab search by the group of Pieter de Jong.

From the RPCI-23 Mouse BAC Library constructed by the group of Pieter de Jong.

VECTOR: pBACe1.
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Pred. No. 7.8e-84;
0; Mismatches 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
/db_xref="taxon:10090"
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/clone_lib="RPCI-23"
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PI JORDAN
PC C12N15/09,C07K14/435,C07K16/18,Lizer...
C12N5/10,
PC C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
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1 (bases 1 to 305)
Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
Edwards,J.B.D.M., Duclert,A. and Lacroix,B.
Par of secretory protein expressed in prostate
Patent: JP 2001512013-A 266 21-AUG-2001;
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JP 2001512013-A/266
21-AUG-2001
31-JUL-1999 JP 2000505291
01-AUG-1997 US 08/905144
JEAN BAPTISTE DUMAS MILNE EDWARDS, AYMERIC DUCLERT, BRUNO
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                                                                                                                                                                                                                                                                 Length 303;
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48.0%; Score 236; DB 6; I
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 236; Conservative 0; Mismatches 0;
                                                                                                         Location/Qualifiers
                                                                                                                                                         1. .303
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                       68. 301.
Location/Qualifiers
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JP 2001512013-A/266.
Homo Bapiens (human)
Homo Bapiens
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AUTHORS
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JOURNAL
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/protein id="CAR01878.1"
/db_xxef="G1:40046204"
/translation="MEHYRXAGSVELPAPSPWPQLPPDTLEWRVRDGSKIRNLLGLAL
GRLEGGSARHVVFSGSGRAAGKAVSCAEIVKRRV"
                                       PAT 18-DEC-2003
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                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 3596 02-OCT-2001;
GENSET
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24-FEB-2000 JP 2000118773
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGTTGGCTCTGGGTCGGTTGGAGGCGCGCAGTCCTCGGCATCTAGTGTTCTCAGGTTCT
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                                                                                                                                                                                                      Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 3603 06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48.0%; Score 236; DB 6; I 100.0%; Pred. No. 2.3e-49; vative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                            68. .. > 301 / note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence tag and encoded human protein. BD027350
BD027350.1 GI:22569092
JP 2001269182-A/3596.
Homo sapiens
                                     DNA
                            303 bp Dl Sequence 3603 from Patent EP1033401.
                                                                                                                                                                                                                                                                                          1. .303
/organism="Homo sapiens"
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                                                                                   AX887740.1 GI:40046203
                                                                                                                     Homo sapiens (human)
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                                                                                                                                         Homo sapiens
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Best Local Similarity
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RESULT 12
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Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Staple, Control, M., Soares, M.B., Bonahdo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullah, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Yillalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: John Ngai, Univ of CA, Berkeley
CDNA Library Preparation: Dr. Sumio Sugano
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: // http://www.shgc.stanford.edu
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LWTQALKEEAATPRHGQRRKRGGTGTGRAEVGGRGKGPRKHPGRPGDTRKPPGHAGGG
QEGMV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAH76268.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 180 Row: j Column: 2
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (06-JUL-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      db_xref="LocusID:436813"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .1554
/organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="zgc:92794"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'gene="zgc:92794"
                                                                                                                                                                                                                                                                                                                                                                      human and mouse cDNA
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Moopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases I to 1554)
Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Altsener, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
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48.0%; Score 236; DB 6; 1
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 236; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
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45. .100
69. .224.
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Danio rerio
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                                                                           identity 97 region 2..2 id R62921
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BC076268
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                                                    216 GAȚTGTCAAGCGGCGGGTCCCAGGCCTGCACCAGCTCACAAGCTACGTTTCCTTCAGAC 275
                                                                                              276 TGAGGACAGCTGGGTCCCAGCCTCACTGACACAGGGCTAGACCCCCTCACAGTGCGCCG 335
                                                                                                                                                                           336 CCATGTGCCTGCAGTGTGGTGCTGCTCAGCCGGGACCCCTGGACCCCAATGAGTGTGG 395
                                                                                                                                                                                           0; Gaps
Best Local Similarity 58.4%; Pred. No. 4.1e-11;
Matches 149; Conservative 0; Mismatches 106; Indels
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Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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MA 02138
Tel: 617-495-1812
Fax: 617-495-857
Email: dmeltonobiohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: 445.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Eutleria; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CER (hoses 1 to 562)
RS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Gradenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Other Este: in44bli.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
M.A. 0213
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/db_xref="taxon:9606"
/clone="IMAGE:6124773"
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/clone libe-"RR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
Not1; Site_2: Xho1; cDNA made by oligo-dT priming.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA linear EST 11-OCT-2002
CDNA clone IMAGE:6124773 5'
PROTEIN. ;, mRNA sequence.
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948407 MA
346756 MA
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UI-CF-FN0
914978 MA
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BU785328.1 GI:23831081
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                 GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                                                - nucleic search, using sw model
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BG328094 111 bp mRNA linear EST 27-FEB-2001 602427145F1 NIH_MGC_15 Homo sapiens CDNA clone IMAGE:4546643 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAATTCGCAACCTGCTG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                     MAGE
                                                                                                                                                                                                                                                 Query Match 100.0%; Score 492; DB 2; I
Best Local Similarity 100.0%; Pred. No. 2.7e-115;
Matches 492; Conservative 0; Mismatches 0;
                                                                                  1. .631
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/orjanism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MA/note="Vector: pBluescriptSKm"
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    Email: johnq@tigr.org
Plate: 111
Seq primer: Reverse.
Location/Qualifiers
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Size-selected on agarose gel. Average insert size -1kb. 5' Ambri site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue. Mb, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Buclid Ave., St. Louis, MO 63110, B-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
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EST369910 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.
AW957840
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1 (bases 1 to 631)
Hegde, P., Qi,R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assessment of gene expression patterns in a model of colon tumor metastasis using a 19,200 element cDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
713 131 833 8528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG
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.larity 100.0%; Pred. No. 2.7e-115;
Conservative 0; Mismatches 0; Indels (
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LOCUS

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/organism="Homo sapiens"
// db_xref="naxon:9606"
// db_xref="naxon:9606"
// clone="InMAGE:30341789"
// iab_host="Bhild Tooh"
// lab_host="Bhild Tooh"
// lab_host="Bhild Tooh"
// lone="Organ: placenta; Vector: pBluescriptR; Site_1:
allx.hol; Site_2: BanH; Oligo-dr primed using primer
5'-TTTTTTTTTTTTTTTVTV-3', size-selected for average
insert size 2.3 kb and normalized to ROT 5. This is a
primary library enriched for full-length clones and
constructed using the Cap-trapper method (Carninci, in
preparation). Library constructed by W. Brownstein
(NIMH/MHGRI, National Institutes of Health). Note: This is
                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gy
Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Mitchael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM373 row: n column: 06
High quality sequence stop: 631.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                    1 (bases 1 to 791)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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             CB959493.1
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                                                                                                                                                                                                                /mol_type="mRNA"
/mol_type="mRNA"
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/note="Organ: colon" Vector: pOTB7; Site 1: XhoI; Site 2:
EcoR1; cDNA made by oligo-dT priming. Directionally
cloned into EcoR1/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size=selected 550bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can life through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 706.
Location/Qualifiers
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/organism="Homo sapiens"
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Genoscope.

Direct Submission

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :

BP 1919 1910 6 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.

Location/Qualifiers
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1 (bases 1 to 888)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
                            CTGCACCAGCTCACCAAGCTTTCCTTCAGACTGAGGACAGCTGGGTCCCCAGCCTCA
                                                                                                                                                                       CCTGACACAGGGCTAGACCCCCTCACAGTGCGCCCCCACATGTGCCTGCTGTGTGGGTGCTG
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                                                                                                                                                                                                                                                                                    CTCAGCCGGGACCCCCTGGACCCCCAATGAGTGTGGTTACCAACCCCCCAGGAGCACCCCCT
                                                                                                                                                                                                                                          CTCAGCCGGGACCCCTGGACCCCCAATGAGTGTGGTTACCAACCCCCCAGGAGCACCCCCT
CTGCACCAGCTCACCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGGTCCCAGCCTCA
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http://fullength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue
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Best Local Similarity 100.0%; Pred. No. 2.8e-115;
Matches 492; Conservative 0; Mismatches 0;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 888)

Li,W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

LD Upublished (2001)

On Feb 13, 2001 this sequence version replaced gi:31066241.

Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

Ist strand cDNA was primed with a Noti-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was dispested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
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888 bp mRNA linear EST 24-MAR-2004
AL528391 Homo sapiens NEUROBLASTOWA COT 25-NORMALIZED Homo sapiens
CDNA clone CSODC029YK21 5-PRIME, mRNA sequence.
AL528391
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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
En (bases 1 to 940)
I (bases 1 to 940)
NIH-MGC http://mgc.nci.nih.gov/.
L Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2527 row: j column: 21
High quality sequence stop: 615.
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AGENCOURT_8485520 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:6305396
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1 (bases 1 to 918)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

4 Unpublished (1999)

5 Contact: Robert Strausberg, Ph.D.

6 Email: Gapbs-romail.nih.gov

7 Tissue Procurement: ATCC

6 CDNA Library Preparation: Life Technologies, Inc.

6 CDNA Library Preparation: Life Technologies, Inc.

7 CDNA Library Preparation: Life Technologies, Inc.

7 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

8 DNA Sequencing by: Agencourt Bioscience Corporation

7 Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

8 High quality sequence stop: 539.

10 Location/Qualifiers

11 Location/Qualifiers
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/tissue_type="epithelioid carcinoma"
/tish_host="Epithelioid carcinoma"
/tish_host="Epithelioid carcinoma"
/clone lib="DHIOB (phage-resistant)"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site 1: Not1;
Ste_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
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                    CTGCACCAGCTCACCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCA
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                                                                                                                                                                                                                                                                                                                                CTCAGCCGGGACCCCCTGGACCCCCAATGAGTGTGGTTACCAACCCCCCGGGAGCACCCCCT
                                                                          GGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTCCCAGGC
                                                                                                                                                                                                                              CCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGGTGCTG
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens
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/tissue_type="1ymphona, cell line"
/lab_host="Numbhona, cell line"
/lab_host="Numbhona, cell line"
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/clone_lib="NIH MGC_99"
/note="Organ: lymph, Vector: pOTB7; Site_l: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/KhoI sites using the following 5' adaptor:
GGCACGACGA(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT [Life Technologies). Note: this is a NIH_MGC
Library."
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AGENCOURT_6773378 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5808601
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             cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bisscience Corporation
Clone distribution: MGC clone distribution information
Clone distribution: MGC clone distribution information
Clone distribution: MGC clone distribution information
Clone distribution: MG.E. Consortium/LLNL at:
http://image.llnl.gov
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100.0%; Score 492; DB 5; I
Best Local Similarity 100.0%; Pred. No. 2.8e-115;
Matches 492; Conservative 0; Mismatches 0;
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ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/Xho1 sites using the following 5, adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
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using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 1000)

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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                           Length 940;
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100.0%; Pred. No. 2.8e-115;
ive 0; Mismatches 0;
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Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BQ056655.1 GI:19815982
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1074)

IN IH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Longublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: DCTD/DTP

CONA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: image.llnl.gov

Plate: LLCMS20 row: k column: 07

High quality sequence stop: 717.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                       BE742621 1074 bp mRNA linear EST 15-SEP-2000 601575430F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3836670 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC 9"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1XhoI sites using the following 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTACCTCCTGATACCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAAACCTGCTG 120
   414 CTCAGCCGGGACCCCCTGGACCCCAATGAGTGTGGTTACCAACCCCCAGGAGCACCCCCT 473
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                                                                                                                                   474 GGCCTGGGTTCCATGCCCAGCTCTGGGCCCTCGTTCCCGAAGAAGAAGAAGAGAC
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100.0%; Score 492; DB 2; Length 10
Best Local Similarity 100.0%; Pred. No. 2.8e-115;
Matches 492; Conservative 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/clone="IMAGE:3836670"
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BE742621.1 GI:10156600
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/lab host="DHIOB (phage-resistant)"
/clone_lib="NIH" (99"
/note="Organ: lymph, Vector: pOTB7; Site_1: XhoI; Site_2:
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
/note_ToTB7; Site_1: 
                                                                                                                                                                                                                                                                           NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Londract: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lou Staudt
cDNA Library Preparation: Rubin Laboratory
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2052 row: o column: 02
High quality sequence stop: 655.
Location/Qualifiers
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                                                                                                                                                                                                     Euteleostomi;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1025)
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/clone="IMAGE:5808601"
                                                              BQ056288.1 GI:19815628
                                                                                                                            Homo sapiens (human)
Homo sapiens
mRNA sequence.
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1104 bp mRNA linear EST 05-MAR-2002
AGENCOURT_6554071 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5555733
5', mRNA Bequence.
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MH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                    54 Arigdaddacraccagaaagcraccacracracaacraccaccaccarraccaa
                                                                                                                                        CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC:
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
                                                   1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG
                                                                                                                                                                                                                                                                                                                          GGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGGGGGGTCCCAGGC
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       Mismatches
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Location/Qualifiers
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/wol type="mrm." saprems
/wol type="mrm." saprems
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ECOR1; CDNA made by oligo-dT priming. Directionally cloned
into EcorI/Xhol sites using the following 5' adaptor:
ECOR1; CDNA made by oligo-dT priming. Directionally cloned
into EcorI/Xhol sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >SOODp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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I (bases 1 to 1079)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                CTGCACCAGCTCACCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGGTCCCCAGCCTCA
                                                                                                                                                                                       CCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTTGGGTGTGGTTG
                                                                                                                                                                                                                                                                                CTCAGCCGGGACCCCCTGGACCCCCAATGAGTGTGGTTACCAACCCCCCAGGAGCACCCCCT
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                                                                                                                                                             CCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTGCTG
                                                                                                                                                                                                                                                      CTCAGCCGGGACCCCTGGACCCCAATGAGTGTGGTTACCAACCCCCAGGAGCACCCCCT
                                                                      CTGCACCAGCTCACCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCA
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can leound through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2097 row: b column: 11
High quality sequence stop: 520.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .1079
/organism="Homo sapiens"
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xrefe="mRNA"
/db_xrefe="taxon:9606"
/clone="LNAGE:592837"
/tissue_type="neuroblastoma, cell line"
/lab hoste-mBHOB (phage-resistant)"
/clone lib="NHH MGC 47"
/note="Organ: brain; Vector: porB7; Site_1: XhoI; Site_2: EcoRI, cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAGG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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K-EST0151955 L5HLK1 Homo sapiens CDNA clone L5HLK1-5-D07 5', mRNA
sequence.
CB110489
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        column: 22
                        High quality sequence stop: 678.
Location/Qualifiers
        Plate: LLCM2090 row: f
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967 bp mRNA linear EST 02-APR-2002

SERNCOURT 6839400 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5922837

5', mRNA sequence.

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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 71"
/note="Organ: uferug; Vector: pCMV-SPORT6; Site 1: Not1;
Site 2: Sal1; Cloned unidirectionally.. Primer: Oligo dT.
Average insert size 2.1 kb.
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Homo sapiens
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 967)
Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTCCCAGGC
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                                                                                                                                          Length 1104;
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100.0%; Pred. No. 2.9e-115;
ive 0; Mismatches 0;
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                                                 /Gell line="HLK-1"
// lab_host="ToplOF" "
// clone llb="LSHKKI"
// clone llb="LSHKKI"
// clone llb="LSHKKI"
// note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI;
Site_2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dr-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coll DNA ligase after digestion of EcoRI which site is a lso included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toplof* by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 604)
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Pred. No. 6.9e-115;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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/clone="L5HLK1-5-D07"
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Best Local Similarity 99.8%;
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        421 GGCCTGGGTTCCATGCCCAGCTCTGTGGCCCTCGTTCCCGAAGAAGGCTCGAGAC
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        489 GGCCTGGTTCCATGCCCAGCTCCAGCTGTGGCCCTCGTTCCCGAAGAAGGGCTCGAGAC
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        481 ACCCGATCGTGA
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1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US106_PUBCOMB.seq:*
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                                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Sequence:
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Maximum DB
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	Description	Sequence 218, App	Sequence 218, App	Sequence 311, App	Sequence 21099, A	Sequence 1, Appli	Sequence 60, Appl	Sequence 920, App	Sequence 52678, A	Sequence 5, Appli	Sequence 5, Appli	Sequence 2039, Ap	Sequence 7620, Ap
	OI.	US-09-731-872-218	US-09-876-997-218	US-09-978-360A-311	US-09-918-995-21099	US-09-981-353-1	US-10-084-817-60	US-10-152-319A-920	US-10-425-115-52678	US-10-037-270-5	US-10-117-722-5	US-09-983-965-2039	US-10-653-047-7620
	图:	Q	10	11	10	σ	15	16	18	15	15	σ	18
	Query Match Length DB	894	894	884	469	1168	1168	260	299	1941	1941	412	929
æ	Query Match	100.0	100.0	98.4	76.0	74.9	74.9	45.5	40.2	15.2	15.2	13.9	8.2
	Score	492	492	484	373.8	368.4	368.4	223.8	197.8	74.6	74.6	68.2	40.4
,	Result No.	-	7	ო	4	n S	9	0 7	80	0	10	11	12

SUMMARIES

US-09-764-877-3291 Sequence 3291, Ap US-10-242-515-3291 Sequence 3291, Ap US-10-156-761-4789 Sequence 1, Appli US-10-126-761-11 Sequence 10, Appli US-10-140-472-10 Sequence 10, Appli US-10-140-472-10 Sequence 10, Appli US-10-140-885-10 Sequence 10, Appli US-10-140-885-10 Sequence 10, Appli US-10-140-923-10 Sequence 10, Appli US-10-140-923-10 Sequence 10, Appli US-10-140-923-10 Sequence 10, Appli US-10-140-865-10 Sequence 10, Appli US-10-140-11-11 Sequence 11, Appli US-10-156-761-121 Sequence 1219, Appli US-10-156-761-121 Sequence 1219, Appli US-10-156-761-121 Sequence 2, Appli US-10-156-761-121 Sequence 2, Appli US-10-132-079-1 Sequence 2, Appli US-10-132-079-1 Sequence 2, Appli US-10-132-115-1884-1 Sequence 2, Appli US-10-132-115-1884-1 Sequence 2, Appli US-09-783-50-3619 Sequence 2, Appli US-09-783-50-3619 Sequence 2, Appli US-09-783-50-3619 Sequence 2, Appli US-09-925-301-2 Sequence 2, Appli US-09-925-301-2 Sequence 2, Appli US-09-925-301-2 Sequence 2, Appli	ALIGNMENTS ean Baptiste UMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS //31,872 69,629 87,470	100.0%; Score 492; DB 9; Length 894; ; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ATGGAGCACTACCGGAAAGCTGGTTGTAGAGCTCCCAGCGCTTCCCCAATGCCCAG 60
US-09- US-10	ALI 731872 7, Jean 1, Jean 7, 709/73 0, 169,	Score Pred. 0, Misr CTGGCTC
	13/09 ardie 1,00 1: 05 1: 05 1	00.0%; ve 0; GGAAAGCT GGAAAGCT GGAAAGCT
32189 32189 32189 9025608 594 594 594 594 594 594 594 594 594 594	ation [126041] 126041] 1.lne Edv. [12604] 1.lne Edv. [127] 1.lne Edv. [127	100.0% ilarity 100.0% Conservative GGAGCACTACCGGAAA(
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$\begin{array}{cccccccccccccccccccccccccccccccccccc$	RESULT 1 US-09-731-872-218 Sequence 218, Application US/09731872 Patent No. US2002012604A1 GENERAL INFORMATION: APPLICANT: Bougueleret, Lydie FULK APPLICATION NUMBER: US 60/169,629 FRIOR FILING DATE: 2000-12-08 FRIOR FILING DATE: 1999-12-08 FRIOR FILING DATE: 2000-03-06 NUMBER OF SEQ ID NOS: 482 SCOTUMARE: Patent.pm SEQ ID NO 218 ILENGTH: 894 ITYPE: DNA ORGANISM: Homo sapiens FRATURE: FRATURE: FRATURE: FRATURE: NAMME/KEY: CDS US-09-731-872-218	1492 192 1
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 US-09-731. Sequence Patence Patence APPLICF APPLICF APPLICF TITLE C FILE R FOURREN CURREN CURREN PRIOR P P P P P P P P P P P P P P P P P P P	Query Best Match
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APPLICANT: Edwards, Jann-Baptiste Dumas Milne
APPLICANT: Bougueleret, Aymeric
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Clusel, Catherine
TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides
FILE REFERENCE: 56.U54.CIP
CURRENT PILING DATE: 1001-10-15
FRIOR APPLICATION NUMBER: US 60/066,677
PRIOR APPLICATION NUMBER: US 60/066,677
PRIOR PELING DATE: 1997-12-17
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: US 60/069,957
PRIOR PELING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: US 60/096,116
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR FILING DATE: 1998-04-13
PRIOR PELICATION NUMBER: US 60/096,116
PRIOR FILING DATE: 1998-11-13
PRIOR PELICATION NUMBER: US 60/096,116
PRIOR FILING DATE: 1998-11-13
PRIOR PELICATION NUMBER: US 09/191,997
PRIOR FILING DATE: 1998-12-17
PRIOR PELICATION NUMBER: US 09/215,435
PRIOR PELICATION NUMBER: US 09/215,435
PRIOR PELICATION NUMBER: US 09/215,155
PRIOR PELICATION NUMBER: US 09/215,155
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PRIOR PELICATION NUMBER: US 09/217,155
PRIOR PELICATION NUMBER: US 09/217,155
PRIOR PELICATION NUMBER: US 09/217,155
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                             CTCAGCCGGGACCCCTGGACCCCAATGAGTGTGGGTTACCAACCCCCAGGAGCACCCCT
                                                                                                                                       258 GCCAGGCTGCAGGAAAGCCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGGGTCCCAGGC
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SOFTWARE: Patent.pm
SEQ ID NO 3111
LENGTH: 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 311, Application US/09978360A Publication No. US20040110939A1 GENERAL INFORMATION:
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US-09-978-360A-311
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Publication No. US20030152921A1

GENERAL INFORMATION:
APPLICANT: Dumas Mine Edwards, Jean Baptiste
APPLICANT: Dumas Mine Edwards, Jean Baptiste
APPLICANT: Dumas Mine Edwards, Jean Baptiste
APPLICANT: JOBERT, Severin
TITLE OF INVENTION: UNBER: US/09/876,997
CURRENT APPLICATION NUMBER: US/09/876,997
CURRENT FILING DATE: 2001-06-08
PRIOR FILING DATE: 2000-12-07
PRIOR PLICATION NUMBER: US 60/187,470
PRIOR FILING DATE: 2000-03-06
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SEQ ID NO 218
LENGTH: 994
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         138 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGAATGGCAGCAAAATTCGCAACCTGCTG
                                                        GGGTTGGCTCTGGGTCGGTTGGAGGCCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT
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100.0%; Score 492; DB 10;
Best Local Similarity 100.0%; Pred. No. 3.4e-140;
Matches 492; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Homo sapiens
; FRATURE:
; NAME/KEY: CDS
; LOCATION: 78..566
US-09-876-997-218
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                                                                     Length 469;
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                                                              Query Match 76.0%; Score 373.8; DB 10; Length Best Local Similarity 99.2%; Pred. No. 4e-104; Matches 386; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020160382A1 184081.24
US-09-981-353-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09981353
Fatent No. US20020160382A1
GENERAL INFORMATION:
APPLICANT: Lasek, Amy W.
TITLE OF INVENTION: GENES EXPRESSED IN COLON CAN;
FILE REFERENCE: PA.0038 US
CURRENT APPLICATION NUMBER: US/09/981,353
CURRENT APPLICATION NUMBER: 2001-10-11
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL PROGram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTCATCCGGGACCCCTGGACCCCCAATG 469
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ORGANISM: Homo sapiens
          sapiens
      ; ORGANISM: Homo E
US-09-918-995-21099
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US-09-981-353-1/c
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                                                                                                                                                                                                                                                                                    Length 884;
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Sequence 21099, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES
FILE REFERENCE: 20411-756
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: PSECSEQ for Windows Version 3.0
SEQ ID NO 21099
LENGTH: 469
                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                  Score 484; DB 11;
Pred. No. 9.3e-138;
8; Mismatches 3;
                             NAMELY, ASTRONOMY OF MENTING MATERIAN OTHER INFORMATION: SCORE 4.6999980926514
OTHER INFORMATION: SCORE 4.6999980926514
OTHER INFORMATION: SEQ LGLALGRLEGGSA/RH
FEATURE:
NAME/KEY: polyA signal
FEATURE:
NAME/KEY: polyA site
1.0CATION: 819..854
1.10CATION: 870..883
US-09-978-360A-311
                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 97.8%;
Matches 481; Conservative
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                       sig_peptide
FEATURE:
NAME/KEY:
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FILE REFERENCE: 44921-5089-US
CURRENT PELING DATE: 2002-05-22
FRICH APPLICATION NUMBER: US 60/292,335
PRIOR FILING DATE: 2001-05-22
PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-06-13
PRIOR PLING DATE: 2001-06-19
PRIOR PLING DATE: 2001-06-19
PRIOR PLING DATE: 2001-06-19
PRIOR PLING DATE: 2001-07-10
PRIOR PLING DATE: 2001-10-22
PRIOR PLING DATE: 2001-11-0-1
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                                                                                                                                 RESULT 7
US-10-152-319A-920/c
S-10-152-319A-920/c
S-10-152-319A-920/c
Publication No. US20040072160A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    Higgs, Brandon
Castle, Arthur
Elashoff, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Rattus norvegicus
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Matches 249; Conservative
                                                     511 CCGATCGTGA 502
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APPLICANT:
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751 GCACCAGCTCACCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACC 692
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                                                     303 TGACACAGGGCTAGACCCCCTCACAGTGCGCCCCATGTGCCTGCAGTGTGGGCTGCTGCT
                                                                                                                                                                CAGCCGGGACCCCCTGGACCCCCAATGAGTGTGGTTACCAACCCCCCAGGAGCACCCCCTGG
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                                                                                                       691 TGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTGCTGCT
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; OTHER INFORMATION: Incyte ID No. US20030119009A1 184081.24
US-10-084-817-60
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US-10-084-817-60/c
; Sequence 60, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
; APPLICANT: Susan Stuart
; APPLICANT: Jasan Stuart
; APPLICANT: Jason M. Shohet
; TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
; FILE REFERENCE: PA-0046 US
; CURRENT APPLICATION NUMBER: US/10/084,817
; CURRENT APPLICATION NUMBER: 60/270,784
; PRIOR APPLICATION NUMBER: 60/270,784
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 365
; SOFTWARE: PERL PROGRAM
; SEQ ID NO 60
; LENGTH: 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Best Local Similarity 99.7
Matches 369; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 TGGCAGCAAAATTCGCAACCTGCTGGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 CCCAGCGCCTTCCCCAATGCCCCAGCTACCTCGTGATACCCTTGAGATGCGGGTCCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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1. Sequence 5, Application US/1011722

2. Publication No. US20030219744A1

3. GENERAL INFORMATION:

4. APPLICANT: Tang, Y. Tom

APPLICANT: Asundi, Vinod

FILE REFERENCE: 784CIP2BCIP

CURRENT APPLICATION NUMBER: US/10/117,722

CURRENT APPLICATION NUMBER: 09/620,312

PRIOR PILING DATE: 2000-07-19

PRIOR PILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1104

SOFTWARE: PL-LGenes Version 1.0

SEQ ID NO 5

LENGTH: 1941
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Pred. No. 1.1e-12;
0; Mismatches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.2%; Score 74.6; DB 15; 57.5%; Pred. No. 1.1e-12; tive 0; Mismatches 99;
                                PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR PLING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SEQ ID NO 5
LENGTH: 1941
              2002-01-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.2%;
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Best Local Similarity 57.5
Matches 134; Conservative
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Best Local Similarity 57.5
Matches 134; Conservative
                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (138)..(773)
US-10-037-270-5
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; LOCATION: (138)..(773)
US-10-117-722-5
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                                                                                                                                                            Sequence 52678, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: About Xihua
APPLICANT: Zhou, Yihua
APPLICANT: APPLICANT: About Xihua
APPLICANT: Con Young
APPLICANT: APPLICANT: About Xihua
APPLICANT: Con Young
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              203 GGGTTGGCTCAGGGTCGGTTAGAGGCGGCAGTGCTCTGCAAGTAGTGCTCTCAGGTTCT 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCACTGCCCCAG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GGGTTGGCTCTGGGTTGGAGGCGGCAGTGCTCGGCATGTAGTAGTGTTCTCAGGTTCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
320 TCCAGCTGTGGTCCCAGACCCCGAAGGAGGCTCGGGACACCCGGTCCTGA 270
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40.2%; Score 197.8; DB 18; Length 299;
Best Local Similarity 94.5%; Pred. No. 2.2e-50;
Matches 205; Conservative 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Education of the control 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGA 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: MRT4577_148039C.1 US-10-425-115-52678
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Felyan
APPLICANT: Chen, Ruil-hong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Zea mays
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LENGTH: 299
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25559 CAAGGAAGCCAGGGTCCCCGGACCACTTCTGCAACCCCAGGGGTGCTGAGGTGCACCTGC 25500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 GGACAGCTGGGTCCCAGCCTCACCTGACACAGGCTAGACCCCCTCACAGTGCGCCGCCA 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               371 ACCCCTGGACCCCAATGAGTGTGGTTACCAACCCCCAGGAGCACCCCTGGCCTGGGTT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       339 TGTGCCTGCAGTGTGGGTGCTGCTCAGCCGGGACCCCCTGGACCCCCAATGAGTGTGTTA 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        305 GCATTGCTGTGCCCTCGCCCAACCAGTCCAAGGTCAACGCCACGAGGCGAGTGCGTTGCGCA 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                365 acticiccicacios de accidades de actividades de 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.2%; Score 40.4; DB 18; Length 929; Best Local Similarity 54.8%; Pred. No. 0.029; Matches 80; Conservative 0; Mismatches 66; Indels 0

    refer to PALM or file wrapper

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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC005
CURRENT APPLICATION NUMBER: US/09/764,877
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapp
NUMBER OF SEQ ID NOS: 4031
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
8.0%; Score 39.4; DB 9; Length 3:
Best Local Similarity 47.1%; Pred. No. 0.078;
Matches 121; Conservative 0; Mismatches 136; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0.029;
Thes 66; Indels
                                              CURRENT APPLICATION NUMBER: US/10/653,047
CURRENT FILING DATE: 2003-08-29
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 1999-03-22
PRIOR FILING DATE: 1999-03-22
NUMBER OF SEQ ID NOS: 7860
SEQ ID NO 7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    425 AGTGCATCAACGACCACTACTTCGTC 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     399 CCAACCCCCAGGAGCACCCCCTGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3291, Application US/09764877
Patent No. US20020147140A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: (1)...(929); OTHER INFORMATION: n = A,T,C or GUS-10-653-047-7620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Tricoderma reesei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-3291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-764-877-3291/c
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Sequence 2039, Application US/09983965

Fatent No. US20020137160A1

GENERAL INFORMATION:
APPLICANT: Warren, Weeley C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND CTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCIE AND FAT DEPOSITION
FILE REFERENCE: 37-21 (10297) C
CURRENT FILING DATE: 2001-10-26
FRICE RAPPLICATION NUMBER: US/09/983,965
FRICE RAPPLICATION NUMBER: US/09/465,231
FRIOR FILING DATE: 1999-12-15
FRIOR PELICATION NUMBER: US 60/113,678
FRIOR PELICATION NUMBER: US 60/113,678
FRIOR FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 5912
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                                                                                                               239 CCCGGGCTCCGGCCCGTTCGCAGACCTGGCGCCGGGCGCGGTGCACATGCGGGTCAAGGA 298
                                                                                                                                                                                                                              96 TGGCAGCAAAATTCGCAACCTGCGTTGGCTTCGGGTCGGTTGGAGGGCGCGCAGTGC
36 CCCAGCGCCTTCCCCAATGCCCCAGCTACCTCCTGATACCCTTGAGATGCGGGTCCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 TCGGCATGTAGTGTTCTCAGGTTCTGGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGA
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Pred. No. 8.8e-11;
0; Mismatches 23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            reredecercaeceradas de de la contra del la contra della c
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APPLICANT: Michael W. Rey
APPLICANT: Jeffrey R.Shuster
APPLICANT: Sakari Kauppinen
APPLICANT: Ib Groth Clausen
APPLICANT: Peter Bjarke Olsen
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
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; OTHER INFORMATION: Clone ID: 26-LIB3057-021-Q1-K1-G5
US-09-983-965-2039
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Publication No. US20040229367A1
GENERAL INFORMATION:
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Best Local Similarity 78.1
Matches 82, Conservative
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US-09-983-965-2039
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   25379 GGCTCCTGGGTCCCGGGGCTTCTGGGTCCCCTTCTCAGGTGCGCCTGGCCACCTTCTGG 25320
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                                                                                                                                                                                                                                                       JULIOLAGE 2151-251/C

Sequence 3291, Application US/10242515
Fublication No. US20040009488A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PCO05C1
CURRENT APPLICATION NUMBER: US/10/22,515
CURRENT PILING DATE: 2002-09-13
FRIOR PELING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR PILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-06-28
PRIOR PELING DATE: 2000-06-28
PRIOR PELING DATE: 2000-06-28
PRIOR PILING DATE: 2000-07-11
PRIOR PELING DATE: 2000-07-11
PRIOR PELING DATE: 2000-07-14
PRIOR PILING DATE: 2000-07-14
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US-10-242-515-3291
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RESULT 15 US-10-156-761-4789/c

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                                                                          APPLICANT: OWURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: IKEDA, HARUO
APPLICANT: BHIKAWA, JUN
APPLICANT: HORIKWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: HATTORI, MASAHIRA
ITILE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-06-02
PRIOR PILING DATE: 2001-06-02
PRIOR PILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 4789
LENGTH: 972
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Sequence 4789, Application US/10156761 Publication No. US20030119018A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Streptomyces avermitilis
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US-10-156-761-4789
                               Publication No. US20
GENERAL INFORMATION:
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Maximum Match 100%
Listing first 45 summaries
                              OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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seq length: 200000000
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                                                                                   Perfect score:
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56: /cgm2_6/ptodata/1/pma/U8101B_COMB.seq;
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50: /cgm2_6/ptodata/1/pma/U8601B_COMB.seq;
50: /cgm2_6/ptodata/1/pm
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| cgn2 6/ptodata/1/pna/US6052_COMB.seq:*
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| cgn2 6/ptodata/1/pna/US6059_COMB.seq:*
| cgn2 6/ptodata/1/pna/US6059_COMB.seq:*
       1117:
1118:
1119:
120:
121:
123:
124:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 172,	4-590 Sequence 590,	7-172 S	7-590 Sequence 590,	5-36232 Sequence 36	80-2683 Sequence 268	8 Sequence 218,	7-218 Sequence 218,	-350 Sequence 350,	0-350 Sequence 350	3-8727 Sequence 8727	8992 Sequence 8992	9-1704 Sequence 1704	9-107 Sequence 107,	3-107 Seguence 107,	3-6569 Seguence 6569	3-7944 Sequence 7944	2-1869 Sequence 1869	869 Sequence 1869	5-353 Sequence 353,	0A-311 Sequence 311,	7-186 Sequence 186,	Sequence 1, A	0-2956 Sequence 2956	3-2956 Sequence 2956,	8-2956 Sequence 2956,	8A-2956 Sequence 2956,	259 Sequence 225	2-2259 Sequence 2259,	2-2259 Sequence 2259,	2A-44786 Sequence 4478	9-99283 Sequence 992	SD-106849 Sequence 106843	09-7116 Sequence 7116, Ap	T-/II6 Sequence /II	0-/IIb	3-39 Sequence 39,	5-132 Sequence 132,	3-33 Sequence 33,	163 Sequence 163,	z-162 Sequence 162,	Z-335 Sequence 335	-335 Sequence 335	
OI 8	03-268	PCT-US03-268	US03-271	PCT-US03-271	8 US-10-170-2	11 US-60-452-	US-09-731-8	e ns-09-816-9	1 US-60-169-6	3 US-60-187-4	8 US-09-649-1	0-669-60-SN	2 US-09-736-1	PCT-US02-051	4 US-09-810-1	8 US-09-649-1	8 US-09-652-9	2 US-09-758-4	US-10-235-9	7 US-09-215-4	US-09-978-3	1 US-60-069-9	3 US-09-770-2	7 US-09-205-0	9 US-09-340-6	7 US-09-898-8	2 US-09-898-8	-09-359-9	0 US-09-359-9	8 US-09-919-0	4 US-09-540-2	4 US-09-540-2	Z-0#6-60-60 #	19 US-09-306-60	2-77C-60-60 7	0-070-0T-00 0	100 0001 100	160 - 200	160-2020-174	FCI - USU2 - USC	FCI-0802-099	0-056-60-S0 T	Z-90T-0T-S0	0 0 0 0 0
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ALIGNMENTS

RESULT 1 PCT-US03-26864-172 ; Sequence 172, Application PC/TUS0326864 ; GENERAL INFORMATION:

APPL: TITLE TITLE TOURRY PRIOD	THERAPEUTICS, INC. METHODS OF USE FOR NOVEL P 0.0013-00304 2003-08-28 MERR: 60/406,616 002-08-29 MERR: 60/406,655 002-08-29 MERR: 60/406,666 002-08-29 MERR: 60/406,611 002-08-17 MERR: 60/406,612 002-08-17 MERR: 60/411,019 002-09-17 MERR: 60/411,046
Query Best Match	Query Match Best Local Similarity 100.0%; Pred. No. 2.4e-110; Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
<i>∂</i> 5 83	1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 60
දු පු	61 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGAAAATTCGCAACCTGCTG 120
65 d	121 GGGTTGGCTCTGGGTTGGAGGCGGCAGTGCTCGGCATGTACTGTTCTCAGGTTCT 180
& q	181 GGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGGGGGGTCCCAGGC 240
<i>&</i> 8	241 CTGCACCAGCTCACCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCA 300
è 8	301 CCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCATGTGCCTGCAGTGTGGGTGCTG 360
& 8	361 CTCAGCCGGACCCCCTGGACCCCAATGAGTGTGGTTACCAACCCCCCAGGAGCACCCCCT 420
č d	421 GGCCTGGGTTCCATGCCGGCTCCAGCTGTGGCCCTCGTTCCCGAAGAAGGGCTCGAGAC 480
& 8	481 ACCCGATCGTGA 492

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GENERAL INFORMATION:

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CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAAAATTCGCAACCTGCTG 120
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Best Local Similarity 100.0%; Pred. No. 2.4e-110;
Matches 492; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                         Sequence 172, Application PC/TUS0327107 GENERAL INFORMATION:
                                                                                                                                               ACCCGATCGTGA 660
                                                                                             481 ACCCGATCGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-27107-172
                                                                                                                                                                                                                                                         RESULT 3
PCT-US03-27107-172
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                                                                                                                                                                   APPLICANT: FIVERRIAD THERAPEUTICS, INC.

TITLE OF INVENTION: METHODS OF USE FOR NOVEL POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES
FILE REFERENCE: 08940.0013-00314
CURRENT FILING DATE: 2003-08-29
PRIOR PELICATION NUMBER: 60/406,616
PRIOR APPLICATION NUMBER: 60/406,655
PRIOR PELICATION NUMBER: 60/406,655
PRIOR PELICATION NUMBER: 60/406,650
PRIOR PELICATION NUMBER: 60/406,650
PRIOR PELING DATE: 2002-08-29
PRIOR PELING DATE: 2002-09-17
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                                                                                                                       Sequence 590, Application PC/TUS0326864 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0
Matches 492; Conservative
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LENGTH: 660
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Sequence 36232, Application US/10170235
Sequence 36232, Application US/10170235
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN.
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF.
FILE REPERENCE: CLOOL330
CURRENT APPLICATION NUMBER: US/10/170,235
CURRENT PILING DATE: 2003-03-17
NUMBER OF SEQ ID NOS: 42514
SEQ ID NO 36232
LENGTH: 889
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100.0%; Pred. No. 2.5e-110;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 492; Conservative
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US-10-170-235-36232
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TITLE OF INVENTION: NOVEL HUMAN POLYPEPTIDES ENCODED BY POLYNUCLEOTIDES
FILE REFERENCE: 08940.0011-00304
FILE REFERENCE: 08940.0011-00304
CURRENT APPLICATION NUMBER: ECT/0803/27107
CURRENT FILING DATE: 2002-08-29
PRIOR PILING DATE: 2002-08-29
PRIOR PLILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: 60/406,655
PRIOR PLILING DATE: 2002-08-29
PRIOR PLILING DATE: 2002-09-29
PRIOR PLILING DATE: 2002-09-29
PRIOR PLILING DATE: 2002-09-19
PRIOR PLILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 60/411,019
PRIOR PLILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 60/411,046
PRIOR PLILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 60/411,046
PRIOR PLILING DATE: 2002-09-17
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                                      GGCCTGGGTTCCATGCCCAGCTCCAGCTGTGGCCCTCGTTCCCGAAGAAGGGCCTCGAGAC
              CTCAGCCGGGACCCCCTGGACCCCAATGAGTGTGGTTACCAACCCCCAGGAGCACCCCCT
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Pred. No. 2.4e-110;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                     Sequence 590, Application PC/TUS0327107 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FIVEPRIME THERAPEUTICS, INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.0%;
Matches 492; Conservative 0
                                                                                                                                                                                                  ACCCGATCGTGA 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
PCT-US03-27107-590
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Sequence 218, Application US/09876997
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78, US4, CIP
CURRENT APPLICATION NUMBER: US/09/876, 997
CURRENT PILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 09/731,872,
PRIOR APPLICATION NUMBER: US 60/187,470
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FILE REFERENCE: 78.US3.REG
CURRENT APPLICATION NUMBER: US/09/731,872
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR FILING DATE: 1999-12-08
PRIOR FILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 482
SOFTWARE: PATENT.PM
LENGTH: 894
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                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                               ; NAME/KEY: CDS
; LOCATION: 78..566
US-09-731-872-218
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GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAs ENCODING POTENTIALLY SECRETED PROTEINS
                                                                                                                           Sequence 2683, Application US/60452680
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: GRUPE, Andrew
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116213
SOFTWARE: FRASEQ for Windows Version 4.0
SEQ ID NO 2681
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ACCCGATCGTGA 492
                      ACCCGATCGTGA 492
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; ORGANISM: Homo sapiens
US-60-452-680-2683
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GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Bougueleret, L.
APPLICANT: Gobert, S.
TITLE OF INVENTION: CDNAS for Secreted Proteins
FILE REFERENCE: 78 INS.PRO.
CURRENT APPLICATION NUMBER: US/60/187,470
CURRENT PILING DATE: 2000-03-06
NUMBER OF SEQ ID NOS: 715
SOFTWARE: Patent.pm
SEQ ID NO 350
LENGTH: 894
                                                                                                 NAME/KEY: sig_peptide
LOCATION: 78. 233
O'THER INFORMATION: VON Heijne matrix
O'THER INFORMATION: seq LGLALGRLEGGSA/RH
FEATURE:
NAME/KEY: polya_signal
LOCATION: 858. 863
FEATURE:
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; LOCATION: 878..894
US-60-169-629-350
                                         78..566
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US-60-187-470-350
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GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Bougueleret, L.
APPLICANT: Jobert, S.
TITLE OF INVENTION: CDNAS for Secreted Proteins
FILE REFERENCE: GENEST: 071PRF
CURRENT APPLICATION NUMBER: US/60/169,629
CURRENT FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 715
SOFTWARE: Patent.pm
SEQ ID NO 350
LENGTH: 894
                                             60/169,629
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 60,
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SEQ ID NO 218
LENGTH: 894
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ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: 78..566
US-09-876-997-218
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US-60-169-629-350
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                         APPLICANT: Goodearl, Andrew D.J.
APPLICANT: Silos-Santiago, Inmaculada
APPLICANT: White, David
APPLICANT: White, David
APPLICANT: White, David
APPLICANT: Busfield, Samantha J.
APPLICANT: Busfield, Samantha J.
APPLICANT: Deeds, James
APPLICANT: Deeds, James
APPLICANT: Busfield, Samantha J.
APPLICANT: Deeds, James
APPLICANT: Busfield, Samantha J.
APPLICANT: Busfi
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GENERAL INFORMATION:
APPLICANT: Curtis, Rory A.J.
APPLICANT: Glos-Santiago, Inmaculada
APPLICANT: DiStefano, Peter
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 492; DB 28; Best Local Similarity 100.0%; Pred.: No. 2.6e-110; Matches 492; Conservative 0; Mismatches 0;
            Villeval, Jean-Luc M.G.
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CRGANISM: Homo sapiens
US-09-649-163-8727
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US-09-699-997-8992
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100.0%; Pred. No. 2.5e-110;
iive 0; Mismatches 0;
                                    Sequence 8727, Application US/09649163
GENERAL INFORMATION:
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Williamson, Mark
Richardson, Jonnifer
MacBeth, Kyle J.
Fraser, Christopher C.
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Galvin, Katherine A.
Leiby, Kevin R.
Kingsbury, Gillian A.
Weich, Nadine S.
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Best Local Similarity 100.(
Matches 492; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-119-1704
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                                                                                                                                                                                                                Length 1086;
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GENERAL INFORMATION:

APPLICANT: Gearing, David P.

APPLICANT: Villeval, Jean-Luc M.G.

APPLICANT: Villeval, Jean-Luc M.G.

APPLICANT: Fraser, Christopher C.

TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES:

TITLE OF INVENTION: THEREFOR

FILE REFREEMENT: 160-2047-001;

CURRENT APPLICATION NUMBER: US/09/736,119

CURRENT FILING DATE: 2000-12-13

FRIOR FILING DATE: 1999-12-13

NUMBER OF SEQ ID NOS: 2118

SOGTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1704
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                            Query Match 100.0%; Score 492; DB 30; Best Local Similarity 100.0%; Pred. No. 2.6e-110; Matches 492; Conservative 0; Mismatches 0;
          FILE REFERENCE: 1600.2020-001
CURRENT APPLICATION NUMBER: US/09/699,997
CURRENT FILING DATE: 2000-10-30
FRICR APPLICATION NUMBER: 60/162,359
FRICR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 12714
SOFTWARE: FASESEQ FOR Windows Version 4.0
SEQ ID NO 89992
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US-09-736-119-1704
; Sequence 1704, Application US/09736119
; GENERAL INFORMATION:
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US-09-699-997-8992
   TITLE OF INVENTION:
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Length 1086;
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TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
FILE REPERENCE: 21272-094-061
CURRENT APPLICATION NUMBER: PCT/USO2/05109
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 09/810,173
Score 492; DB 32;
Pred. No. 2.6e-110;
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                                                                                            0; Mismatches
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Ma, Yunging
Yamazaki, Victoria
Chen, Rui-hong
Wang, Zhiwei
    100.0%;
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Wang, Jian-Rui
Wang, Dunrui
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Zhou, Ping
Goodrich, Ryle
Asundi, Vinod
Zhang, Jie
Zhao, Oing A.
Ren, Feiyan
Xue, Aidong J.
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         Query Match
Best Local Similarity 100.
Matches 492; Conservative
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121 GGGTTGGCTCTGGGTCGGTTGGAGGGGGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 180
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    APPLICANT: Ghosh, Malabika J.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: Novel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 804
CURRENT APPLICATION NUMBER: US/09/810,173
CURRENT FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 526
SOFTWARES PL FL Genes Version 2.0
SEQ ID NO 107
LENGTH: 1089
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                            ; NAME/KEY: CDS
; LOCATION: (275)..(763)
US-09-810-173-107
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APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Goodrich, Ryle
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jiae
APPLICANT: Zhang, Jiae
APPLICANT: Zhao, Qing A.
APPLICANT: Chen, Rui-hong
APPLICANT: Chen, Rui-hong
APPLICANT: Wehrman, Tom
APPLICANT: Wehrman, Tom
APPLICANT: Wang, Yonghong
APPLICANT: Wang, Yonghong
APPLICANT: Wang, Yonghong
APPLICANT: Wang, Zhiwei
APPLICANT: Wang, Dunrui
PRIOR FILING DATE: 2001-03-15
NUMBER OF SEQ ID NOS: 1052
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 107
LENGTH: 1089
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                                                                                                           TYPE: DNA
ORGANISM: Homo sapiens
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NAME/KEY: CDS
LOCATION: (275)..(766)
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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUG_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUG_COMB.seq:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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198 GGTTGCCTCTGGGTCGGTTGGAGGCGCCAGTGCTCCGGCATGTAGTGTTCTCAGGTTCT

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GECAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTCCCAGGC 317

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241

CTGCACCAGCTCACCAACGAACGTTTCCTTCAGAGCAGGACAGCTGGGTCCCAGCCTCA

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33584, 34304, 111296 1123, Ag 111, 7 111, 7 113386 11385, 11385, 11385,		Gaps CCCAG CCCAG TGCTG TGCTG
Sequence Seq		Length 461; Indels 0; GCCTTCCCCAATGC GCTTCCCCAATGC CAAAATTGGCAACC CAAAATTGGCAACC
US-09-489-039A-3584 US-09-680-312D-501 US-09-270-77-11298 US-08-845-998-5 US-09-430-845-5 US-09-430-845-5 US-09-430-845-5 US-09-430-845-5 US-09-445-247-11 US-09-445-247-11 US-09-445-247-11 US-09-45-2912A-6 PCT-US96-06231A-3864 US-09-252-991A-13854	ULT 1 09-621-976-217 equence 217, Application US/09621976 atent No. 6639063 APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Dumas Milne Edwards, J.B. APPLICANT: Giordano, J.Y. APPLICANT: SET and Encoded Human Proteins. FILE REFERENCE: GENSET. 054PR2 CURRENT PILING DATE: 2000-07-21 CURRENT PILING DATE: 2000-07-21 NUMBER OF SEQ ID NOS: 19335 SOFTWARE: Patent.pm ERGTH: 461 TYPE: DNA ORGANISM: Homo sapiens FEATURE: NAME/KEY: 619 ORGANISM: 18. 461 LOCATION: 78. 461 LOCATION: 78. 233 OTHER INFORMATION: secq LGLALGRLEGGSA/RH OTHER INFORMATION: secq LGLALGRLEGGSA/RH	Score 374.4; DB 4; Pred. No. 7.4e-98; 2; Mismatches 4; SCTGGCTCTGTAGAGCTCCCAGC
4 4	us/o ward and 1PR2 1PR2 15 - 07 15 - 07 15 - 07 15 - 07 15 - 07 15 - 07	76.1%; 98.4%; ive CGGAAA CGGAAA ACCCTT
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10000000000000000000000000000000000000	ULT 1 09-621-976-217 equence 217, Application US/096 attent No. 6639063 ENERAL INFORMATION: APPLICANT: Dumas Milne Edwards, APPLICANT: JODGTL, S. APPLICANT: Giordano, J.Y. TITLE OF INVENTION: ESTS and ENFILE REFERENCE: GENSET, 054PR2 CURRENT FILING DATE: 2000-07-2 NUMBER OF SEQ ID NOS: 19335 SOFTWARE: PATENT: 2000-07-2 NUMBER OF SEQ ID NOS: 19335 EQ ID NO 217 LENGTH: 461 TYPE: DNA TYPE: DNA TYPE: DNA TYPE: MAWE/KEY: sig_peptide LOCATION: 78461 NAWE/KEY: sig_peptide LOCATION: 78233 OTHER INFORMATION: seq_LGLALGR 07THER INFORMATION: seq_LGLALGR	σω
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SOFTWARE: PERL Program
SEQ ID NO 92
LENGTH: 2375
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ORGANISM: Homo sapiens
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; NAME/KEY: CDS
; LOCATION: (138)..(773)
US-09-620-312D-5
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ORGANISM: Homo sapiens
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CTGCACCAGCTCACCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCA 377
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Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PILE REFERENCE: 59. US2. REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTHARE: PATENCE DE NOS: 36681
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                                                                                                              CTCAGCCGGGACCCCCTGGACC 382
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Sequence 5, Application US/09620312D
Patent No. 656966;
GENERAL INFORMATION:
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APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Chen, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Zhao, Qing A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wehrman, Tom
Xue, Aidong J.
Yang, Yonghong
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ORGANISM: Homo sapiens
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LOCATION: 68.301
US-09-513-999C-3603
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Sequence 92, Application US/09976594

Sequence 92, Application US/09976594

Sequence 92, Application US/09976594

Sequence 92, Application US/09976594

Setting Application No. 6673549

TITLE OF INTERNITE PRINCE ENCRY. BUCHING SERVESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS FILE REFERENCE: PA-0041 US

CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2001-10-12

PRIOR FILING DATE: 2000-10-12
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# APPLICANT: anou, r.i.s

APPLICANT: May Yunging

APPLICANT: Mang, bunrul

APPLICANT: Wang, Dunrul

APPLICANT: Wang, Dunrul

APPLICANT: Wang, Dunrul

APPLICANT: John Tillinghast

TITLE OF INVENTION: No. 656962el Nucleic Acids and

TITLE OF INVENTION: No. 656962el Nucleic Acids and

TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 784CTP2B

CURRENT APPLICATION NUMBER: US/09/620,312D

CURRENT APPLICATION NUMBER: 09/552,317

PRIOR PILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-04-25

PRIOR FILING DATE: 2000-01-21

NUMBER OF SEQ ID NOS: 1105

SOFTWARE: PL_Genes Version 1.0

SEQ ID NO 5

LENGTH: 1941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 74.6; DB 4;
Pred. No. 7.8e-12;
0; Mismatches 99;
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NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. 6673549 337221.11

US-09-976-594-92
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                                                                                                                                                                 96 TGGCAGCAAAATTCGCAACCTGCTGGGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGC 155
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Patent No. 6703491

GENERAL INFORMATION

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SECTION SET PATENTIN Ver. 2.0

SEQ ID NO 23492

LENGTH: 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8210
                                                                             36 CCCAGCGCCTTCCCCAATGCCCCAGCTACCTCCTGATACCCTTGAGATGCGGGTCCGAGA
                                                                                                                                                                                               156 TCGCCATGTAGTGTTCTCAGGTTCTGCCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGA
                                      Gaps
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                                    Indels
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             Pred. No. 8.4e-12;
0; Mismatches 99
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57.5%; Pre-
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; ORGANISM: Drosophila melanogaster
US-09-270-767-8210
           Local Similarity 57.5
nes 134; Conservative
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ZIP: 53701-2113

COMPUTER READABLE FORM:
COMPUTER: DISKette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
COMPUTER: Word Perfect 8.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION ATA:
PRIOR APPLICATION DATA:
                                                                               Length 356;
                                                                             Query Match 9.3%; Score 46; DB 4; Length 356 Best Local Similarity 51.5%; Pred. No. 0.00067; Matches 106; Conservative 0; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plunkett, Guy
Welch, Rod
TITLE OF INVENTION: No. 6365723el Sequences of E.
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Seay, Nicholas J.
REGISTRATION UNBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 GCTGAGATTGTCAAGCGGCGGGTCCC 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 GCCGAGGTCCTCAAGCGGAGCCACCC 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-17
US-09-453-702B-72/c
; Sequence 72, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
APPLICANT: Blattner, Frederick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burland,
) OKGANISM: Drosophila melanogaster
US-09-270-767-23492
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STRANDEDNESS: double
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17179

17239

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17240 GCATTGCCACGGGTAAAGTTGGGCAGGAGGCTGCATCCACACTTTCACCCGGTGGGTTC 17299
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               56 CCCAGCTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAATTCGCAACC
                                                                    116 TGCTGGGGTTGGCTCTGGGGTCGGTTGGAGGGCGGCCAGTGCTCGGCATGTAGTGTTCTCAG
                                                                                                                                                                                          17180 TGATGCAACTGGATGGCGTTGGCGCATAGCCGTTATTGCGTACCAGATCGTCTGCGCG
                                                                                                                                                                                                                                                      176 GITCTGGCAGGCTGCAGGAAAGGCTGTCTGCGCTGAGATTGTCAAGCGGCGGGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08690473
Patent No. 5876923
GENERAL INFORMATION:
APPLICANT: Leopardi, Rosario
APPLICANT: Roizman, Bernard
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 AS AN
TITLE OF INVENTION: INHIBITOR OF APOPTOSIS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IEM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,473
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Pred. No. 1.7;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARCD: 239
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ATTORNEY AGENT INFORMATION:
NAME: Highlander, Steven L.
REGISTATION NUMBER: 37,642
REFERENCE/DOCKET NUMBER: ARCD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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MEDIUM TYPE: Floppy
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nes 78; Conserv
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COUNTRY: USA
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US-08-690-473-1
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Matches
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                                                                                                                         56 CCCAGCTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACC
                                                                                                                                                                                                                                            116 TGCTGGGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGTGTTCTCAG
                                                                                                                                                                                                                                                                                                                                                               GTTCTGGCAGGGCTGCAGGAAAGGCTGTGCGCTGAGATTGTCAAGCGGCGGGTCC
                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Welch, Rod TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
            DB 3; Length 46819;
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COUNTRY: US

ZIP: 53701-2113

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 8.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,7028
FILING DATE: 03-Dec-1999
CLASSIFICATION: <UNKNOWN>
      Score 37.2; DB 3; Length 4. Pred. No. 1.2; 0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 7.2%; Score 35.6; DB 3; Length 2 Best Local Similarity 48.5%; Pred. No. 2.6; Matches 98; Conservative 0; Mismatches 104; Indele
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REGISTRATION WUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 251:
18-09-453-702B-251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
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Patent No. 6365723
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGGCCTGCACCAGCTCACCAA 257
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Perna, Nicole T.
Plunkett, Guy
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STRANDEDNESS: double
      7.6%;
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INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
Query Match
Best Local Similarity 49.0
Matches 99; Conservative
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Sequence 11., Application US/08458568A
Settle No. 5821339
GENERAL INFORMATION:
APPLICANT: Schaffer, Priscilla A.
APPLICANT: Yeh, Lily
TITLE OF INVENTION: Compositions and Methods for Treatment of Herpesvirus
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APPLICANT: LEOPARDI, ROSANIO
APPLICANT: LEOPARDI, BERNARD
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
FILE REPERENCE: ARCD: 31708C1
CURRENT APPLICATION NUMBER: US/09/825,288A
CURRENT FILING DATE: 2001-04-02
PRIOR PILING DATE: 1999-03-01
PRIOR PILING DATE: 1996-03-01
PRIOR PILING DATE: 1996-07-26
SOFTWARE: PATENTING DATE: 1996-07-26
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                                                                                                                                                                                                                                                                                                                                                                          Length 4257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                71; Indels
                                                                                                                                                                                                                                                                                                                                                                     Score 35.4; DB 3;
Pred. No. 1.7;
0; Mismatches 71;
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         TYPE: nucleic acid

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                     7.2%;
Local Similarity 52.3%;
nes 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-458-568A-11/c
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                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                 APPLICANT: LEOPARDI, ROSARIO
APPLICANT: LEOPARDI, BERNARD
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
TITLE OF INVENTION: HERPES SIMPLEX VIRUS ICP4 IS AN INHIBITOR OF APOPTOSIS
CURRENT APPLICATION NUMBER: US/09/259,821A
CURRENT FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 08/690,473
PRIOR PILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET: 2.1
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Patent No. 6218103
GENERAL INFORMATION:
APPLICANT: Leopard, Roasrio
APPLICANT: Leopard, Bernard
ITILE OF INVENTION: HERPES SIMPLEX VIRUS US3 AND ICP4 AS
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
7.2%; Score 35.4; DB 3;
Best Local Similarity 52.3%; Pred. No. 1.7;
Matches 78; Conservative 0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2404 récededededecedededes 2432
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ATTORNEY/AGENT INFORMATION: NAME: Highlander, Steven L. REGISTRATION NUMBER: 37,642
REPERENCE/DOCKET NUMBER: ARSB:519
TELECHONE: (512) 418-3000
TELEPAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
                                                                                                                                                                    Sequence 1, Application US/09259821A
Patent No. 6210926
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: HERPES VIRUS, TYPE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4257
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                                                                                                                        US-09-259-821A-1
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SEQ ID NO 1
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TILE REPERENCE: 514412A-2005.1
CURRENT APPLICATION NUMBER: US/09/727,238
CURRENT FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: 09/319,892
PRIOR PILING DATE: 1999-06-14
PRIOR PILING DATE: 1999-106-14
PRIOR FILING DATE: 1997-12-03
PRIOR FILING DATE: 1997-12-03
PRIOR FILING DATE: 1997-12-05
PRIOR FILING DATE: 1997-12-05
PRIOR FILING DATE: 1996-12-06
NUMBER: OF EQ ID NOS: 4
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390 GTGTGGTTACCAACCCCC 407
                FILING DATE: 1998-06-24
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                                                            NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver.
SEQ ID NO 2
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                                                                                                                                                                                                                          LENGTH: 4403765
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US-09-727-238-1
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%5-genence 2, Application US/09103840A

%5-genence 2, Application US/09103840A

% Patent No. 659431

% GENERAL INFORMATION:

% APPLICANT: FLEISCHMAN, Robert D.

% APPLICANT: WITTE, Owen R.

% APPLICANT: VENTER, John C.

% TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

TITLE OF INVENTION: TUBERCLOSIS

% FILE REFERENCE: 24366-20007.00

% CURRENT APPLICATION NUMBER: US/09/103,840A
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                                                                                                                                                   ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz & No. 5821339ris
STREET: One Liberty Place, 46th floor
CITY: Philadelphia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Worderfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: 05/08/458,568A
FILING DATE: 05/08/1995
CLASSIFICATION: 435
RIGHTOR APPLICATION: 435
RILING DATE: 05-MAY-1993
CLASSIFICATION: 435
FILING DATE: 05-MAY-1993
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Leary Ph.D., Kathryn R.
REGISTRATION NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 36,317
REFERENCE/DOCKET NUMBER: 36,317
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFOR
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STRAIN: Herpes Simplex Virus Type 1
INVENTION: Infections
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INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                      NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock,
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Best Local Similarity
Matches 78; Conserva
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Sequence 1, Application US/09727238

Patent No. 6555733

GENERAL INFORMATION:
APPLICANT: Bartsch, et al.
TITLE OF INVENTION: No. 6555733el genes coding for amino acid deacetylases with spec:
TITLE OF INVENTION: acetyl-L-phosphinothricin, their isolation and their use.
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FEATURE:
OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1317)
COTHER INFORMATION: N-acetyl-PPT deacetylase coding sequence
US-09-727-238-1
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No. 1.7; Matches 96; Conservative 0; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 7.2%; Score 35.2; DB 3; Length 4 Best Local Similarity 71.9%; Pred. No. 19; Matches 46; Conservative 0; Mismatches 18; Indels
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Search completed: January 31, 2005, 18:09:29 Job time : 98 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

January 26, 2005, 14:52:01; Search time 32.6 Seconds (without alignments) 481.084 Million cell updates/sec Run on:

US-10-057-813-14 861 1 MEHYRKAGSVELPAPSPMPQ.....SMPSSSCGPRSRRRARDTRS 163 Title: Perfect score: Sequence: Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ΙD	Description
	219.5	25.5	538	2	H86335	T20H2.2 protein -
7	105.5	ď	369	7	F96788	protein T4012.22 [
ო	86.5	10.0	350	~	C26984	probable requiator
4	85.5		906	7	T00039	hypothetical prote
2	84.5		368	~	T35150	probable glycosyl
9	84		397	~	T30168	hypothetical prote
7	84	9.8	634	7	T00388	cal
89	82.5	9.6	556	~	D70940	probable PPE prote
თ		9.5	1275	7	AD0332	probable membrane
10	81	o,	367	~	C39590	TPA-induced protei
11	80.5		257	7	T10586	small nuclear ribo
12	80.5	6	495	Н	P2WLB2	L2 protein - bovin
13	80	σ.	589	~	C70767	probable pknJ - My
14	79.5	σ.	1052	7	T00067	hypothetical prote
15	79	6	469	-	P2WLB	L2 protein - bovin
16	79	σ,	770	~	G70718	probable cation tr
17	78.5	ο,	359	7	T36443	probable penicilli
18	78.5		579	~	C75599 .	TerF-related prote
19	78.5		2605	~	T18552	saframycin Mx1 syn
20	78	٠	817	~	S51342	verprolin - yeast
21	78	9.1	827	~	H83217	probable transcrip
22		•	6420	0	T30283	polyketide synthas
	76.5	•	467	~	T34874	hypothetical prote
	76.5	8.9	474	~	T19543	hypothetical prote
	76.5	•	1460	Н	EDBEIF	immediate-early pr
26	76.5	8.9	2142	~	B35098	MHC class III hist
	16	8.8	202	N	AF2088	hypothetical prote
28	16	٠	434	-	WMBEF3	
59	9/	8.8	537	0	153719	NF-kappa-B transcr

microtubule-associ	breast cancer susc	hypothetical prote	araC-family transc	probable benzoate	amidohydrolase (im	probable hydrolase	RHR2 protein - yea	triose-phosphate i	hypothetical prote	flagellar basal bo	hypothetical prote	immediate-early pr	GAP-associated pro	CDA peptide synthe	rRNA (adenine-N6-)
A43359	T42207	D72532	T44488	F75566	AH3100	B98186	S48426	T31319	B72677	D30930	T08794	A45344	A38218	T36248	T17408
0	N	~	~	~	~	~	~	~	~	~	~	-	7	~	7
2774	3343	231	405	433	466	466	271	278	307	260	565	1446	1493	7463	336
8.	8.8	8.8	8.8	8.8	8.8	8.8	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7	8.7
92	16	75.5	75.5	75.5	75.5	75.5	75	75	75	75	75	75	75	75	74.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 H86335 T20H2.2 protein - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: H86335 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.R.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Hulzar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon, A;Tile: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Accession: H86335 A;Accession: H86335
A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-538 <5TO> A; Cross-references: UNIPROT:Q9LNUS; GB: AE005172; NID:g8778978; PIDN: AAF79893.1; GSPDB:G C; Genetics: A; Map position: 1 Query Match Best Local Similarity 30.4%; Pred. No. 4.6e-12; Matches 55; Conservative 31; Mismatches 64; Indels 31; Gaps 6;
Qy 1 MEHYRKAGSVELP-APSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSG 59
 Qy 120 LLSRDPLDPNECGYQPPGAPPGLGSMPSSSCGPRSRRARDT 161 bb 334 TLSKEQLNTSSVGYQCPIPIEMVKPLABIDYEGQDGSPRGRRGRGGRGRGRGG 391 Qy 162 R 162 Db 392 R 392
 RESULT 2 P96788 protein T4012.22 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: F96788

```
hypothetical protein KIAA0290 - human (fragment)
C;Species: Homo sapiens (man)
R;Odara, O.; Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Nomura, N.
R;Ohara, O.; Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Nomura, N.
A;Description: Prediction of the coding sequences of unidentified human genes.
A;Reference number: Z14073
A;Reference number: Z14073
A;Accession: T00039
A;Accession: T00039
A;Accession: T00039
A;Residues: 1-906 <OHA
A;Residues: 1-906 <OHA
A;Cross-references: UNIPROT:O14526; EMBL:AB006628; NID:d1170681; PIDN:BAA22959.1; PID:d1
C;Genetics:
A;Note: KIAA0290
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LRFLQTEDSWVPASP-- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        433 PRTSSCAE----RLQSEEQVSKNLFGPPLESAFDHEDFTGSSSLGFTSSPSPFSSSSPEN 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --DTGLDPLTVRRHV-----PAVWVLLSRDPLDPNECGYOPPGA----PPGLGSMP---S 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489 VEDSGLDSPS---HAAPGPSPDSWVPRPGTPQSPPSCRAPPPEARGIRAPPLPDSPQPLA 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable glycosyl transferase - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004
C;Accession: T35150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47 LPVPGDWPR--PD-----DAARAELARVLRRLPDGAV--VLLDG-----LVACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 PAPSPMPQLPPD--TLEMRVRDGSKIRNLLGLALGRLEGGS-ARHVVFSGSG-----RAA
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A;Reference number: 221570
A;Accession: T33150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53;
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A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
9.9%; Score 85.5; Di
Best Local Similarity 26.5%; Pred. No. 9.2;
Matches 49; Conservative 17; Mismatches
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Matches 46; Conserv
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Chin, C.W.; Chung, M.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, ansen, N.F.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. Rizzo, M.; Rooney, T.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Accession: F96788
A; Accession: F96788
                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-369 <STO>
A,Cross-references: UNIPROT:Q9LQR7; GB:AE005173; NID:g8778814; PIDN:AAF79819.1; GSPDB:GN
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Cincession: C2694
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Cincession: C2694
Nucleic Acids Res. 15, 8041-8056, 1987
Aritle: Gene cluster for streptomycin biosynthesis in Streptomyces griseus: nucleotide Aritle: Gene cluster for streptomycin biosynthesis in Streptomyces griseus: nucleotide Aritle: Gene cluster for streptomycin biosynthesis in Streptomyces griseus: nucleotide Aritle: Gene cluster for streptomycin biosynthesis in Streptomyces griseus: nucleotide Aritle: Gene cluster A93676; MUID:88040426; PMID:3118332
Aricession: C2698
Aricession: C26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Streptomyces griseus
Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MDKYQR------VVKPKADTPIDANEIRITSQGRARNYITYAMTLLQVFNESEMCQFTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  53 RHVVFSGSGRAAGKAVSCAEIVKRRVP-GL-----HQLTKLRFLQTEDSWVPASPD--T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----SKIRNLLGLALGRLEGGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GGSARHVVFSGSGRAAGKAVSCAEIVK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 GLDPLTV-----RRHVPAVWVLLSRD----PLDPNE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLSAKTVGTLRSCSTAGVPQSNVRIGRDGRARPLDPTE 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable regulatory protein 5 - Streptomyces griseus C; Species: Streptomyces griseus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 105.5; DB
; Pred. No. 0.055;
17; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MEHYR--KAGSVELPAPSPMPQLPPDTLEMRVRDG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVPGLHOLTKLRFLQTEDSWVPASPDTGLDP 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
10.0%; Score 86.5; Di
Best Local Similarity 29.1%; Pred. No. 2.7;
Matches 46; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 22.5*
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Gene: T4012.22
A, Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77
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probable PPE protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Accession: D70340
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamilin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Hamilin, N.; Holroyd, S. Nature 393, S37-554, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Aritle: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUD:98295987; PMD:9634230
A;Accession: D70940
A;Residues: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-556 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:053678; GB:AL021929; GB:AL123456; NID:g3242291; PIDN:CAA173 A;Experimental source: strain H37Rv C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable membrane protein YPO2724 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Species: Versinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD032
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Reference number: AB0001; MUD:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8ZD68; GB:AL590842; PIDN:CAC92963.1; PID:g15980702; GSPDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 BIVKRRVPGL-----HQLTK-----LRFLQTEDSWVPA-SPDTGLDPLTVRHVPAVW 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 SCAEIVKRRVPGLHQLTKLRFLQTEDSWVP---ASPDTGLDPLTVRRHVPAV-----WV 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 SVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.5%; Score 81.5; DB 2; Length 1275;
Best Local Similarity 36.1%; Pred. No. 30;
Matches 22; Conservative 11; Mismatches 15; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.6%; Score 82.5; DB 2; Length 55 Best Local Similarity 26.0%; Pred. No. 10; Matches 38; Conservative 20; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               488 YLDLDP----ETGHDPTGSPQGAGTL 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 LLSRDPLDPNECGYQPPGAPPGLGSM 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 V 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: PPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a
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                                                                                                        C) Accession: T30168
R) Latreille, P.; Wammaley, P.; Kramer, J.

Rubmitted to the BMBL Data Library, November 1996
A) Description: The sequence of C. elegans cosmid F26B1.

A) Reference number: 220748
A) Accession: T30168
A) Accession: T30168
A) Accession: T30168
A) Accession: T30168
A) Residual type: DNA
A) Residual type: DNA
A) Residual type: DNA
A) Residual type: DNA
A) Cross-references: UNIPROT: P91277; EMBL: U80444; PIDN: AAB37791.1; GSPDB: GN00019; CESP: F2
A) Experimental source: strain Bristol N2; clone F26B1
A) Genetics:
A) Genetics:
A) Genetics:
A) As Dosition: 1
A) A: Introns: 16/3; 40/2; 78/3; 93/2; 117/3; 320/3; 382/2
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A;Experimental source: brain
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein KIAA0616 - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 0.1Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00388
R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N. DNA Res. 5, 169-176, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete A;Reference number: Z14142; MUID:98403880; PMID:9734811
A;Accession: T00388
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 FLQTEDSWVPASPDTGLDPLTVRRH-----VPAVWVLLSRDPLDPNECGYOPPGAPPGL 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDT---GLDPLTVRRHVPAVWVLLS--- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   302 SSPQHRPAGVSPLSLSTEARRQQASPTLSPLSPLSPTQAVAMDALSLEQQLPYAFFTQAGSQ 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31 RDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAVSCAEIVKRRVPGLHQ--LTKLR 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 SVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAV 68
hypothetical protein F26B1.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76; Indels 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----RDPLDPNECGYOPP-----GAPPGLGSMPSSSC--GPR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 9.8%; Score 84; DB 2; Length 634; Best Local Similarity 22.0%; Pred. No. 8.5; Matches 37; Conservative 23; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.8%; Score 84; DB 2
Best Local Similarity 26.5%; Pred. No. 5.1;
Matches 35; Conservative 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 GGAITQGGGQRS 265
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A;Molecule type: DNA
A;Residues: 1-495 <GRO>
A;Cross-references: UNIPROT:P06457; GB:X01768; GB:M24326; NID:g60859
C;Cross-references: UNIPROT:P06457; GB:X01768; GB:M24326; NID:g60859
C;Superfamily: papillomavirus L2 protein
C;Keywords: glycoprotein; late protein
F;28,459,478/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                Query Match
9.3%; Score 80.5; Di
Best Local Similarity 23.8%; Pred. No. 13;
Matches 38; Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: C70767
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                                                          TPA-induced protein 11D - mouse
C;Species: Mus musculus (house mouse)
C;Species: 30-Aug-1991 #sequence_revision 30-Aug-1991 #text_change 09-Jul-2004
C;Accession: C39590
R;Varnum, B.C.; Ma, Q.; Chi, T.; Fletcher, B.; Herschman, H.R.
Mol. Cell. Biol. 11, 1754-1758, 1991
A;Title: The TISI1 primary response gene is a member of a gene family that encodes prote
A;Reference number: A39590; MUID:91141531; PMID:1996120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: T10586
R; Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke submitted to the Protein Sequence Database, June 1999
R; Bevan, M.; Pohl, T.; Weizenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke submitted to the Protein Sequence Database, June 1999
A; Accession: T10586
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-257 < BEV>
A; Residues: 1-257 < BEV>
A; Residues: 1-257 < BEV>
A; Cross-references: UNIPROT: O9SUNS; EMBL: ALO80253; GSPDB: GN00062; ATSP: F9F13.90
A; Experimental source: cultivar Columbia; BAC clone F9F13
A; Gene: ATSP: F9F13.90
A; Map position: 4
C; Superfamily: proline-rich protein
                                                                                                                                                                                                                                                                                                                            A,Molecule type: mRNÁ
A,Residues: 1-367 <VAR>
A;Cross-references: UMIPROT:P23949; GB:M58564; NID:g202066; PIDN:AAA72946.1; PID:g202067
C;Keywords: DNA binding; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              small nuclear ribonucleoprotein-associated protein homolog F9F13.90 - Arabidopsis thalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --- GRLEGGSARHVVFSGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---- QLTKLRFLQTEDSWVP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Arabidopsis thaliana (mouse-ear cress)
Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 protein - bovine papillomavirus type 2
5Species: bovine papillomavirus type 2
5Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97 VPASPDIGLDPLIVRRHVPAVWVLLSRDPLDPNECGYQPPGAPPGLGSMPSSSCGP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 ASPDIGLDPLIVRRHVPAVWVLLSRDPLDPNECGYQP-----GAPPGLGSMP 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.4%; Score 81; DB 2 ilarity 37.5%; Pred. No. 8.7; Conservative 6; Mismatches
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R;Groff, D.B.; Mitra, R.; Lancaster, W.D.
submitted to GenBank, May 1988
A;Reference number: A94519
A;Accession: B31169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 QLPPDTLEMRVRDGSKIRNLLGLAL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GRAAGKAVSCAEIVKRRVPGLH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 PPPFGGOGP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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Matches
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hypothetical protein KIAA0453 - human (fragment)
C;Species: Homo sapiens (man)
C;Jate: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 09-Jul-2004
C;Accession: 700067
R;Seki, N; Ohira, M.; Nagase, T.; Ishikawa, K.; Miyajima, N.; Nakajima, D.; Nomura, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable pknJ - Mycobacterium tuberculosis (strain H37RV)

() Species: Mycobacterium tuberculosis

() Species: Mycobacterium tuberculosis

() Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

() Accession: C70067

R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Parkhill, J.; Garnier, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A;Authors: Sqares, R.; Barrell, B.G.

A;Atthors: Sqares, R.; Barrell, B.G.

A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: Mycobacterium tuberculosis probable serine/threonine-specific protein kin F;13-276/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-589 <COLD. A;Residues: 1-589 <COLD. A;Experimental source: UNIPROT:Q10697; GB:Z73966; GB:AL123456; NID:g3261577; PIDN:CAA98200 A;Experimental source: strain H37Rv
                                                                                     9
                                                                                                                                                                                                                                                                                                                         51 SARHVVFSGSG-----RAAGKAVSCAEIVKRRVPG-----LHQLTKLRFLQTEDSWVPAS 100
                                                                                                                                                                                                                                                                                                                                                                             98 SPRYVPLRTSGSTTSLASVGSRAGAATGTRSSITGIPLDTLETIGALRPGAYEDTVLPEA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 PEVLAGQGFDGRADLYSLGCALFRLLTGEAPFAAGAGAAVAVVAGHLHQPPPTVSDRVPG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81 L-------BQLTKLRFLQTEDSWVPASPDTGLDPLTVRRH 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292
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                                                                                                                                                                                                                                            97
                                                                                                                                                                   ---GRL-EGG
                                                                                                                                                                                                                                            44 YRTCKQAGTCPPDVIPKVEGDTI-----ADKILKLGGLAIYLGGLGIGTWSTGRVAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23 PDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRA--AGKAVSCAEIVKRRVPG
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                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 APHV---ISQGAVPGSPWWQHPVGSVTALATPPGHGWPPGLPPLPRRPRRYR 341
                                                                                 39;
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    Length 495;
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                                                                             62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            101 P-----DTGLDPLTVRRHVPAVWVLLSRDPLDPNE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158 PAIVTPDAVPADTGIDGLSIGTDSSTETLITLLEPEGPED 197
                                                                                                                                                          4 YRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLAL-
DB 1;
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C;Accession: A03653
R;Chen, E.Y.; Howley, P.M.; Levinson, A.D.; Seeburg, P.H.
Nature 299, 529-534, 1982
A;Title: The primary structure and genetic organization of the bovine papillomavirus typ. A;Reference number: A93289; MUID:83012974; PMID:6289124
A;Accession: A03653
A,Title: Characterization of cDNA clones in size-fractionated cDNA libraries from human A,Reference number: Z14085; MUID:98116662; PMID:9455484
A,Accession: T00067
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-1052 < SERS
A,Cross-references: UNIPROT:09UIMO; EMBL:AB007922; NID:d1225331; PIDN:BAA32298.1
C,Genetics: A,Note: KIAA0453
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A;Residues: 1-469 < CHE>
A;Cross-references: UNIPROT:P03109; GB:X02346; GB:J02044; GB:M24622; GB:X00473; NID:g609
C;Superfamily: papillomavirus L2 protein
C;Keywords: late protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                59 GSGRAAGKAVSCAEIV-----KRRVPG----LHQLTKLRFLQTEDSWVPASPD 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 SPRYTPL----RTAGSTSSLASIGSRAVTAGTRPSIGAGIPLDTLETLGALRPGVYEDTV 125
                                                                                                                                                                                                                                                                                                                                                                                                                             19 POLPP-DILEMRVRDGSKI-----RNLLGLA----LGRLEGGSARHVVFS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 YRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLAL------GRL-EGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 YRTCKOAGTCPPDVIPKVEGDTI-----ADKILKFGGLAIYLGGLGIGTWSTGRVAAGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 SARHVVFSGSGRAAGKAVSCAEIVKRRV----PGLHQLTKLRFLQT------EDSW 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 protein - bovine papillomavirus type 1
Species: bovine papillomavirus type 1
Bate: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 VPASP-----DTGLDPLTVRRHVPAVWVLLSRDPLDPNECG---YQPPGAP 139
                                                                                                                                                                                                                                                                                                           Query Match
9.2%; Score 79.5; DB 2; Length 1052;
Best Local Similarity 25.2%; Pred. No. 37;
Matches 40; Conservative 20; Mismatches 36; Indels 63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 9.2%; Score 79; DB 1; Length 469
Best Local Similarity 24.4%; Pred. No. 17;
Matches 43; Conservative 19; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TGLDPLTVRRHVPAVWVLLSRDP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             399 KPSAARSTEGSAILDIAGLAAVTDNRYEP----LMLRKP 433
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Job time : 34.6 secs
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                                                                     Q8b139 mus musculu
Q93h39 streptomyce
Q8cgw4 mus musculu
Q9kz7 streptomyce
G6ka19 mus musculu
Bad21438 mus musculu
                                                                                                                                                                                Q811e7 mus musculu
P08076 streptomyce
Q8vd37 mus musculu
Q8ky52 azospirillu
 Q8ved2 mus musculu
                                  oryza sat
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                   Q6zay3 or
Bac99602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Straubberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032136; AAH32136.1; -.
Genew, HGNC:19909; C90-F123.
Interpro; IPR011574; Alba DUF78.
ProDom; PD010497; Alba DUF78; 1.
SEQUENCE 163 AA; 17631 MW; 442C8727191A0BCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Chromosome 9 open reading frame 23 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 861; DB 2; 100.0%; Pred. No. 1.5e-66;
                                                                                                                                                                                                                                                                                                                                                                                             163 AA
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                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                           Q6KAL9
BAD21438
Q811E7
STRR STRGR
Q8VD37
                   Q6ZĀY3
BAC99602
Q94JH5
Q8BL39
Q93H39
SX30 MOUSE
CNO MOUSE
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=C9orf23;
                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2002
01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1 MEHYRKAGSVELPAPSPMPQ.....SMPSSSCGPRSRRRARDTRS 163
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Q6dgs1
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               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                  1825181 segs, 575374646 residues
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Maximum Match 100%
Listing first 45 summaries
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Q7XT90
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Q9M8Z6
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Q8IDN4
Q7RPX4
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Q7YWL9
Q7RVU1
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MISTAIR ST., Fearingold B.A., Grouse L.H., Derge J.G.,

Altachal S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,

Altachal S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marushia K., Farmer A.A., Rubin G.M., Hong L.,

A Loptelon M., Soares M.B., Bonado M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Rapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,

Rapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,

Rapleton M., Soares M.B., Garcia A.M., Gay L.J., Hulyk S.J.,

Richards S.,, McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Yourigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Gren E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

"Gones S.J., Marra M.A.;

"Gones S.J., Marra M.A.;

"Temenation and initial analysis of more than 15,000 full-length human and initial analysis of more than 15,000 full-length human
                                                                                                      MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS 60
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                                                                  GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.7%; Score 815; DB 2; Length 163; larity 94.5%; Pred. No. 1.4e-62; Conservative 3; Mismatches 6; Indels
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Strausberg R.,
Maritan A. Maritan R.,
Maritan
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nl protein.
163 Aa; 17675 MW; 87675201AF87F5B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JOCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (RIKEN cDNA 2810432D09).
Name=2810432D09Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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SEQUENCE 16
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GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
                                                                                                             61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPTSPDTGLDPLTVRRHVPAVWVL 120
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STRANT-GSTBL/GJ TISSUE-Whole body;
The FANTOW CONSORTIUM,
The RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
Manalysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630 (2000).
                     MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810432D09 product:hypothetical protein, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-CSTBL/6J; TISSUE-Whole body,
MEDLINE-20530913; PubMed=1107686;
MEDLINE-20530913; PubMed=1107686;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsuncto H., Sakaguchi S., Itogami T., Kashimagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashiraki Y.;
SRIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                 LSRDPLDPNECGYQPPGAPPGLGSMPSSSCGPRSRRRARDTRS 163
                                                                                                                                                                                         STRAIN=CSTBL/60; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
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                                                                                                                                                                                                                                                                                                                     163
                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 17, Created)
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STRAIN=CS7BL/6J; TISSUE=Whole body;
MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-CS7BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM CONSCRIUM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Meth. Enzymol. 303:19-44(1999)
                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2003 (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           insert sequence.
Name=2810432D09Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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and mouse cDNA sequences.
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       Jones S.J., Marra M.A.;
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                                                                           SEQUENCE FROM N.A.
TISSUE=Brain;
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                                                                                                                                                                                                                                                                                                                                                                                                                         R 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R 181
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                                                                                                                                                                                                                                                                                                          23
                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                           Query Match
Best Local
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Q91WE3
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Klausher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

By Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rhiching R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                     Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramateu M., Hayashizaki Y.,
Bubmitted (UUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
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                                                                                                                                                                                                                                                                                                                                                                                         1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
NOBI TaxID=7955;
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                                                                                                                                                                                                                                                                                                                                  Length 163;
                                                                                                                                                                                                                                                                                                                                                                6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 LSRDPLDPNECGYQPPGAPPGLGSMPSSSCGPRSRRARDTRS 163
                                                                                                                                                                                                                                                                                                      163 AA; 17648 MW; DC89421F4F617429 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                  Score 814; DB 2;
Pred. No. 1.8e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             224 AA
                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                            MGD; MGI:1917211; 2810432D09Rik.
InterPro; IPR011574; Alba DUF78.
ProDom; PD010497; Alba DUF78; 1.
 Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                94.5%;
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                                                                                                                                                                                                                                                                                                                                                             Matches 154; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                        protein.
                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                        Hypothetical
                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                  Query Match
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"Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                -----RHVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASP
                                                                                                                                                                                                                                                                                                                                                                                      102 DIGLOPLIVRRHVPAVWVLLSRDPLDPNECGYOPPGAPPGL--GSMPSSSCGPR-SRRRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DCT-2004 (TrEMBLrel. 28, Last annotation update)
Ribonuclease P 25kDa subunit (Mus musculus ES cells cDNA, RIKEN full-
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                         22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     length enriched library, clone:C330033C13 product:hypothetical
protein, full insert sequence).
                                                                                                                                                                                                                    Length 224;
                                                                                                                                                                                                                                                         46; Indels
                                                                                                        Strausberg R.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL: BC076268, AAH76268.1;
Hypothetical protein.
                                                                                                                                                               (1 protein.
224 AA; 24369 MW; C2FD38C9D8B2F38A CRC64;
                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mouse cDNA sequences.";
c. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                ch 48.9%; Score 421; DB 2; Similarity 47.5%; Pred. No. 2.2e-28; 86; Conservative 27; Mismatches 46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 AA.
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40.7%; Scor
43.6%; Preditive 25;
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     Query Match
Best Local Similarity 43.6
Matches 75; Conservative
                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=Skin;
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                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=RPP25;
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Q9BUL9
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EMBL; ECO16085; AAH16085.1; —.
                                                                                                                                                                                                                                                                                                                                                                                                                                           the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Nuramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sawi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., RIKEN integrated sequence analysis (RISA) system-384-format Sequencing pipeline with 384 multicapillary sequence:";
                                                                                                                                                                                                                                                                                                                           "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                              Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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199 AA; 21037 MW; B9DE105BE3293D64 CRC64;
                                                                                                                                                                            Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J;
MEDLINE=20499374; PubMed=11042159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J;
MEDLINE=20530913; PubMed=11076861;
                                                                                                                                                          MEDLINE=99279253; PubMed=10349636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MGD; MGI:2143151; AI851155.
InterPro; IPR011574; Alba_DUF78.
ProDom; PD010497; Alba_DUF78; 1.
                                                                                                                                                                                                                                                                                                             RIKEN FANTOM Consortium;
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                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
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                                                                                                                     SEQUENCE FROM N.A.
                         SEQUENCE FROM N.A.
                                                                                                                                         STRAIN=C57BL/6J;
                                                              Strausberg R.;
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SEQUENCE 19
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TISSUESERIAIN, and Skin;

TISSUESERIAIN, and Skin;

MEDLINE-22388257; PubMed=12477932;

Katausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhar N.K.,

Altschul S.F., Zeeberg B. B., Buerow K.H., Schaefer C.F., Bhar N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heise F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., Mozhey R.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Wilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley W.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                         51 SARHVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSW--VPASPDTGLDP- 107
                                                                                                           1 MEHYRKAGSVELPA-----PSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGG
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=21998191; PubMed=12003489;
Guerrier-Takad C., Eder P.S., Gopalan V., Altman S.;
Guerrier-Takad C., Eder P.S., Gopalan V., Altman S.;
Furification and characterization of Rpp25, an RNA-binding protein subunit of human ribonuclease P.";
RNA 8:290-295(2002)
RNA 8:200-295(2002)
EMBL; BC002497; AAH02497.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                         121 DPAASLSVLKAVVPSLAILLSKDALDPRQLGYQPPNLSPGPSSPPTVSTSKRS 172
                                        18;
                                                                                                                                                                                                                                                 108 ----LIVERHVPAVWVLLSRDPLDPNECGYQPPGAPPGLGSMPSSSCGPRS
2; Length 199;
                                        54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sci. U.S.A. 99:16899-16903(2002).
Score 350; DB 2;
Pred. No. 2.6e-22;
5; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPP25 protein (RNase P protein subunit p25).
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01-MAY 2000 (TrEMBLrel. 13, 01-CT-2002 (TrEMBLrel. 22, 01-MAR-2004 (TrEMBLrel. 26, CG9422-PA (CG9422-PC).
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                                                                                                                                                                                             SARHVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSW--VPASPDTGLDP- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SARHVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLIKLRFLQTEDSW--VPASPDTGLDP- 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEHYRKAGSVELPA-----PSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGG 50
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                                                                                                                                                                                                                                                    ----LTVRRHVPAVWVLLSRDPLDPNECGYQPPGAPPGLGSMPSSSCGPRS 154
                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----LTVRRHVPAVWVLLSRDPLDPNECGYQPPGAPPGLGSMPSSSCGPRS 154
                                                                                                                 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQUENCE FROM N.A.

SEQUENCE FROM N.A.

Tanigami A., Pujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K. Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK000381; BAA91128.1; -.

InterPro; IPR011574; Alba DUF78.

ProDom; PD010497; Alba DUF78; 1.

SEGUENCE 199 AA; 20660 MW; 855494F0366B2291 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.4%; Score 339; DB 2; Length 199; 41.9%; Pred. No. 2.3e-21; ive 26; Mismatches 56; Indels
                                                                                      Length 199;
                      InterPro; IPR011574; Alba DUF78.
ProDom; PD010497; Alba DUF78; 1.
SEQUENCE 199 AA; 20632 MW; 9A4494F0297B2A81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
ENSANGE0000016002 (Fragment).
Name=ENSANGG0000013513;
                                                                                 39.8%; Score 343; DB 2;
42.4%; Pred. No. 1.1e-21;
tive 26; Mismatches 55,
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EMBL; AY034074; AAK54443.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein FLJ20374.
                                                                                              l Similarity 42.4%;
73; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 72; Conserv
                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
               ntAct; Q9BUL9;
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REAL MEDLINE=20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

Liu X., Mattei B., McIntosh T.C., McLeod M.P., McDecken D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 SGSGRAAGKAVSCAEIVKRRVPGLHQLTKL--RFLQTEDSWVPASPDTGLDPLTVRRHVP 115
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                       STRAIN=PEST;
Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary databases.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 215;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215 215
215 AA; 24004 MW; AA72B25FAA8ABFBE CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 30.5%; Score 263; DB 2; Similarity 39.6%; Pred. No. 9.4e-15; 65; Conservative 28; Mismatches 61;
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Stapleton M., Carlson J., Chavez C., Frise E., Ge
Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
                                                         114 VPAVWVLLSRDPLDPNECGYQPPGAP----PGLGSM---
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                                                                                                                                                          153 RSRRRARDTRS 163
                                                                                                                                                                                                            178 RPNKRTRPGRN 188
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                                                                                                                                                                                                                                                                                                                                    Q6NNC7
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OGNNC7
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RA Mount S.M., Molshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Rahazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Saith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., RA Svifekas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Wang Z.Y., Wassarman D.A., Wehnstock G.M., Weissenbach J., RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao G., The genome sequence of Drosophila melanogaster.";

I. The genome sequence of Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----LPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-2242665; PubMed=12537568; Carlson J.W., Halpern A Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., Pacel S., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfelifer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Glbbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.4%; Score 235.5; DB 2; Length 206; 33.0%; Pred. No. 2.1e-12; ive 27; Mismatches 70; Indels 31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AE003790; AAM70814.1; -.
IntAct, Q9V9B6; -.
Flybase; FBDM0033092; CG9422.
SEQUENCE 206 AA; 23146 MW; 9FCFDF4C3C9BC5D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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MEDLINE=22426070; PubMed=12537573;
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---PSSSCGP 152
                                                    118 IPTLHILMSLDELPDTIDGLQKPNTSTDFWDGGGAQQQPHPRSQPRHQQQPHKPGAGRGG 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 IPTLHILMSLDELPDTIDGLQKPNTSTDFWDGGGAQQQPHPRSQPRHQQQPHKPGAGRGG 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 VPAVWVLLSRDPLDPNECGYOPPGAP----PGLGSM-----------PSSSCGP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Berkeley; Stapleton W., Carlson J., Chavez C., Frise E., George R., Pacleb J., Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J., Bark S., Wan K., Yu C., Rubin G.M., Celniker S.; Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BT011363; AAR96155.1; ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31,
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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta, Pterygota,
Booptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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SGRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWV 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sakano H., Vaysberg M., Lee J.M., Lenz C., Liu S., Pham P., Toriumi M., Yu G., Chin C., Chiou J., Choi E., Chung M., Gonzalez A., Howng B., Liu A., Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R., Federapiel N.A., Theologis A.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

PIR: H86335; H86335.
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
4x1976010/T4012_22.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicacee, Arabidopsis.
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ProDom; PD010497; Alba DUF78; 1.
SEQUENCE 538 AA; 58572 MW; 1B0BB141F0F9AF22 CRC64;
                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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t; Pred. No. 1.5e-10;
31; Mismatches 64;
                                                                                                                                                                     538 AA
                                                                                                                                                                                                                                  Created)
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(TrEMBLrel. 15, I
(TrEMBLrel. 26, I
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l Similarity 30.4%;
55; Conservative 33
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01-MAR-2004 (TrEMBLrel.
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               169 R 169
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                                                                                                                                                                                                                                                                                                                                                                                                             61 CVVWSGSGGGVVKIICCAEVLKRSHP-LYQVTRMAYTSVEEHWKPQM--EGLEEIIVTRQ 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 VPAVWVLLSRDPLDPNECGYQPPGAP----PGLGSM-------PSSSSCGP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 HVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRH 113
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                                                                                                                                                                                                                                                                                                              1 MMHYRKAENVEKELSKSDLPPEDCMPKSQKDFLWMHVKGGTKVSNVIEFAQEALNKGEHR
                                                                                                                                                                                                                                                 1 MEHYRKAGSVE-----LPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSAR
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Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                              31;
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                                                                                                                            26.8%; Score 230.5; DB 2; Length 20
32.5%; Pred. No. 5.7e-12;
ive 27; Mismatches 71; Indels
      to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases
EMBL; BT011363; AAR96155.1; -.
SEQUENCE 206 AA; 23162 MW; 8B9FD01C279BC5D9 CRC64;
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INCENTRO; IPRO11574; Alba DUF78.
ProDom; PD010491; Alba DUF78; 1.
SEQUENCE 315 AA; 33763 MW; 6DC486E51238A937 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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178 RPNKRTRPGRN 188
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                                                                                                                                                           Similarity
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                                                                                                                            Query Match
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Oliveira A.C., Mattos L.T., Carvalho F.F., Shimano A., Zimmer P.D., Malone G., Dellagostin O.; Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AB109206; BAC79194.1;

Gramene; Q7XJ13; -...
Gramene; Q7XJ13; -...
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0005608; F:Peperain A activity; IEA.
GO; GO:0005608; P:proteolysis and peptidolysis; IEA.
InterPro; IPR011574; Alba DUF78.
InterPro; IPR001461; Peptidase A1.
InterPro; IPR001461; Peptidase A1.
InterPro; IPR00169; Peptidase A1.
ProDom; PF00005; Asp. Aba DUF78; I.
ProSITE; PS00141; ASP_FROTEASE; UNKNOWN_2.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

NCBI_TaxID=39947;

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61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
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                                                                                                                                                                                                                                                                                                                                        Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.9%; Score 206; DB 2; Length 350; 29.9%; Pred. No. 1.3e-09; vative 23; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                            Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases
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LSKIELNTSSVGYQCPIPIELVKPMGDIDYEGREGSPGGRG-
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InterPro; IPR011574; Alba DUF78.
ProDom; PD010497; Alba DUF78; 1.
SEQUENCE 350 AA; 37383 MW; D
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Best Local
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QYXJ13; 01-0CT-2003 (TrEMBLrel. 25, Created) 01-0CT-2003 (TrEMBLrel. 25, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Chloroplast nucleoid DNA-binding protein-like protein. Name=P047BE02.13; Oryza sativa (japonica cultivar-group).

SEPTER

732 AA.

PRT;

PRELIMINARY;

Q7XJ13 ID Q7XJ13

RESULT 15

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GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LSRDPLDPNECGYQPP-----GAPPGLGSMPSSSCGPRSRRARDTR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602 LSKKELDTSSIGYOSPLPADKVKPLVEYENEEDAPSPAGRGRGRGGGGGGGGGGGGTG 659
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                                                                                                                                                                                                                                                DNA-binding.
SEOUENCE 732 AA; 78353 MW; 7EA86DD5386374AC CRC64;
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FEATURE:
NAME/KEY: SIGNAL
 RESULT 1
US-09-621-976-4077
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LOCATION:
NAME/KEY: 1
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Sequence 39818, A
Sequence 25927, A
Sequence 18806, A
Sequence 17504, A
Sequence 19363, A
Sequence 23623, A
Sequence 23623, A
Sequence 28830, A
Sequence 28830, A
Sequence 28830, A
Sequence 2110, A
Sequence 23620, A
Sequence 23620, A
Sequence 23620, A
Sequence 23621, Appl
Sequence 23, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 19, Appl
                                                                     January 26, 2005, 14:52:47; Search time 41.4407 Seconds (without alignments) 260.851 Million cell updates/sec
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                                                                                                                                         1 MEHYRKAGSVELPAPSPMPQ......SMPSSSCGPRSRRARDTRS 163
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-09-513-999C-7680
US-09-270-76-7681
US-09-270-76-7681
US-09-252-991A-28916
US-09-252-991A-19363
US-09-252-991A-19363
US-09-252-991A-28836
US-09-252-991A-28830
US-09-252-991A-28830
US-09-252-991A-28830
US-09-252-991A-28965
US-09-252-991A-28978
US-09-410-551B-21
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US-09-940-316B-23
US-09-940-316B-23
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Maximum Match 100%
Listing first 45 summaries
                                                  protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Maximum DB
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GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4077, Application US/09621976
GENERAL ND. 6639063
GENERAL INFORMATION:
APPLICANT: Johert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION:
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF ESQ ID NOS: 19335
SOFTWARE: PATENT UP
US-09-252-991A-31100
US-09-252-991A-32578
US-09-252-991A-16723
US-09-252-991A-32604
US-09-252-991A-31758
US-09-252-991A-31758
US-09-252-991A-31758
US-09-252-991A-31758
US-09-252-991A-31768
US-09-252-991A-31800
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US-09-621-976-4077
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900-7680
Sequence 7680, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
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UNSURE
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Patentin Ver. 2.0
SOFTWARE: Patent
SEQ ID NO 55035
LENGTH: 118
                                                                                                                                                                           Query Match
                                                          TYPE: PRT
                                                                                                FEATURE:
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Sequence 39818, Application US/09270767

Patent NO. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nuclea acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 6227

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 39818
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Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7336-094
CURRENT PELLION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517
                                                                                                                                                                                                                                                                                                                                                                                           1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                                                                                                                                                                             1 DLPFEDCMPKSOKDFLWMHVKGGTKVSNVIEFAQEALNKGEHRCVVWSGSGGGVGKTISC
  APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US 60/122,487

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm
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                                                                                                                                                                                                                                                                                                            Query Match
45.9%; Score 395; DB 4; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.6e-35;
Matches 78; Conservative 0; Mismatches 0; Indels
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41.8%; Pred. No. 7.6e-09;
iive 16; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-39818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||::|| | |:|::::
61 AEVLKRSHP-LYQVTRMAY 78
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Best Local Similarity 41.8%
Matches 33; Conservative
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US-09-270-767-55035
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US-09-270-767-39818
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Sequence 18806, Application US/09252991A
Fatent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 00/074,788
FRICR APPLICATION NUMBER: US 60/074,788
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APPLICANT: Narc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-7
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 25927
FENGTH: 050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                385 OVRRRSDPAARORPGV------ATGDPGPRPATORRTAPGLRTGRPQH 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 PSPMPQLPPDTLEMRVRDGSKIRNLLGLALG--RLEGGSARHVVFSGSGRAAGKAVSCAE 72
                                                                                                                                                                                                                    70
                                                                                                                                                                                                                                           11 ELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAVSC
                                                                                                                                                                     Gaps
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                                                                                                                 Length 118;
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                                                                                                                 17.6%; Score 151.5; DB 4;
41.8%; Pred. No. 7.6e-09;
iive 16; Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 -- DPLDPNECGYQPPGAPPGLGSMPSSSCGPRSRR 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25927, Application US/09252991A Patent No. 6551795
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                ||::|| | |:|:: : 61 AEVLKRSHP-LYQVTRMAY 78
                                                                                                                                                                                                                                                                                                                      71 AEIVKRRVPGLHQLTKLRF 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-25927
                                                                                                                                                                        33; Conservative
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Best Local Similarity
Matches 40; Conserv
                                                                                                                                              Best Local Similarity
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US-09-252-991A-18806
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US-09-252-991A-25927
                                                                     US-09-270-767-55035
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USCALABLE OF 187-20363

Sequence 20363, Application US/0925291A

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: USRG1186.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 20363

LENGTH: 429
                                                               Sequence 19363, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US 60/074,788
PRIOR PRILING DATE: 1998-02-18
PRIOR PRILING DATE: 1998-02-18
PRIOR PRILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 GQAAPGKRRARRQRPRRPGRHAGSLGQRRSGIPEGAWRGPRPGPPGRSPSPAPR---- 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 LPÁGLRGGPVGALPAVDLHARRADLPRRRLRVPLOGOÁGOAAHLGOGVHRRFAGGDLLPG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 RKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAA 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 10.5%; Score 90.5; DB 4; Similarity 27.3%; Pred. No. 0.12; 44; Conservative 12; Mismatches 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.5%; Score 90; DB (Best Local Similarity 31.3%; Pred. No. 0.2; Matches 51; Conservative 11; Mismatches
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US-09-252-991A-20363
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Best Local Similarity
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PELICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17504
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; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-17504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43 ALGRIEGGSARHVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPD 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GRRPGLGAVPLS---PAARR 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 TGLDPLTVRRHVPAVWVLLSRDPLDPNECGYQPPGAPPGLGSMPSSSCGPRSRRR 157
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                                                                                                                                                                                                                                                                        Query Match 10.6%; Score 91; DB 4; Length 345; Best Local Similarity 25.7%; Pred. No. 0.12; Matches 45; Conservative 12; Mismatches 38; Indels
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18806
LENGTH: 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               334 HLGRLARHVAGDRAGPRSERRA 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 A-PELSGOGRRHLRDAAGGRRSGLA
                                                                                                                                                                                       ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18806
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179 RGAGR-----LHRRHPGGEPQLRRRPAGL-DRAVPAVLRPGPD----RLHPARLHLA 226

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US-09-252-991A-19831

is Sequence 19831, Application US/09252991A

is Sequence 19831, Application US/09252991A

is Patent No. 6551795

is Title OF INVENTION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERRINCE: 107196.136

CURRENT RILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER: OF SEQ ID NOS: 33142

LENGTH: 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICATION APPLICATION US/09252991A

RACERT NO. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1999-07-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
--- AEQGTLRHPAGAGSARRPGPRTSAAPGR 205
                                                                                                                                                    ---RAGGDRGRAALRLRRGAGAAAIAAARLLRAGETELP 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 AGALRSPADRP------RRVRQ----RGRAGLAPG--PAGGRRHAAAAVGGRTDAL 286
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                                                                        75 KRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRD--
                                                                                                                                                                                                                                                                            126 LDPNECG-----YQP-PGAPPGLGSMPSSSCGPRSRRARDTR 162
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Best Local Similarity 26.9%; Pred. No. 0.65;
Matches 52; Conservative 8; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      287 RRREHRVRAVAGRA-SCLRHLSRRRPA-----
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    165 PDGAPELPADSRP-
                                                                                                                                                        206 RGRGPGROP----
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US-09-252-991A-27110
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Facet No. 651795

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

FILE REFERENCE: 107196.136

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 374

TYPE: PRI

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                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Warc J. Rubenfield et al.
APPLICANT: Warc J. Rubenfield et al.
APPLICANT: Warc J. Rubenfield et al.
APPLICANT: WARC J. RUBENFIELD ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23622
LENGTH: 4322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AARRHGRÄGRAPG------HPPWPVRRPRGGQPPGPGADLRRTDPB--LCRTRC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 PSPMPQLPPDTLEMRVR-----DGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAV 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 PRPAPRLLPDLQPRPVRRTAHRADGRTLAEPAGGAAGR----PAAAHCRIAAVRRGAEAT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 PSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAVSCAEIV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels 41; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 89.5; DB 4; Length 432; ; Pred. No. 0.23; 13; Mismatches 68; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 PLDPN------ECGYQPPGAPPGLGSMPSSSCGPRSRRAR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 PLOPSGARPAOSRRRPGSAGRPGPGAFAGDGRRPAGD--POGRRRLR 151
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10.1%; Score 87; DB 4; Length 374;
Best Local Similarity 24.6%; Pred. No. 0.35;
Matches 41; Conservative 11; Mismatches 63; Indels
                                            --MPSSSCGP-RSRR 156
                                                                                                                227 DHEDRRPPAGAHARPGAPAGVGAAGDHRGGQPVDAAGPCRDRR 269
                                                                                                                                                                                                                                                                                                        Sequence 23622, Application US/09252991A Patent No. 6551795
                                        122 SRDPLDPNECGYQPPGAPPGLGS-
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Best Local Similarity 26.9%;
Matches 45; Conservative 13
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US-09-252-991A-28830
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US-09-252-991A-23622
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; NAME/KEY: UNSURE
; LOCATION: (338),(413)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-28965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 GSARHVVFSGSGR-AAGKAVSCAEIVKRRVPGLHQLTKLRFLQTEDSWVPASPDTGLDPL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 GTP---VGAGQGHPAAG-----AL 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          109 TVRRHVPAVWVLLSRDPLDPNECGYOPPGAPPGLGSMPSSSCGPRSRRARDTR 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              248 SAQRQEPA--AAAQRSPRRSAAAG-QPRGTHRA-GIRPAVSEGRRQRLVARPRR 297
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.9%; Score 85; DB 4; Length 441; Best Local Similarity 27.0%; Pred. No. 0.72; Matches 47; Conservative 14; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: January 26, 2005, 15:08:51
Job time : 42.4407 secs
                         PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FLILNG DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 28965 LENGTH: 441
     1999-02-18
BER: US 60/074,788
                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
       FILING DATE:
                                                                                                                                                                                                                                                         FEATURE
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TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
SEQ ID NOS: 33142
SEQ ID NOS: 33142
LENGTH: 497
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
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                                                                                                                                                                                                                                                                                                               97 VPASPDTGLDP-----LTVRRHVPAVWVLLSRDPLDPNECGYQPPGAPPGLGSMPSS 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351 RROSRLRHLHLRLHRPA------EGRĞQHPRGA----GRAPAMDAGHLRPRRRR 394
                                                                                                                                                                           43 ALGRIE-GGSARHVVFSGSG-----RAAGKAVSCAEIVKRRVPGIHQLTKIRFLQTEDSW 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 POLPPDTLEMRV-----RDGSKIRNLLGLALGRLEG---GSARHVVFSGSGRAAGKAVSC 70
                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                               35;
                                                                                                                                                                                                                            338 ATGRLHPGGGRRRMARAVAGPREPVRPGAPAGAAGGAGGRRAPGLYQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.9%; Score 85.5; DB 4; Length 497; 26.9%; Pred. No. 0.74; tive 10; Mismatches 52; Indels 73
                                                                        Query Match 9.9%; Score 85.5; DB 4; Length 477; Best Local Similarity 29.1%; Pred. No. 0.71; Matches 39; Conservative 11; Mismatches 49; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23620, Application US/09252991A Patent No. 6551795 GENERAL INFORMATION:
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Patent No. 6551795
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                149 SCGPRSRRRARDTR 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 26.9%
Matches 49; Conservative
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- protein search, using sw model OM protein

January 26, 2005, 14:52:01 Run on:

; Search time 18.2 Seconds
(without alignments)
481.084 Million cell updates/sec

1 MEHYRKAGSVELPAPSPMPQ......BIVKRRVPGLHQLTKLRFLQ US-10-057-813-14_COPY_1_91 Perfect score: Sequence:

91

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

2: pir2:* 3: pir3:* 4: pir4:* PIR 79:* 1: pir1:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES 짪

ip	T20H2.2 protein -	protein T4012.22 [Ω			protein	small nuclear ribo	calcium-dependent	conserved hypothet	hyperosmolarity-re	dihydrolipoamide d	breast cancer susc	serine/threonine-s	conserved hypothet	hypothetical prote	probable SF16 prot	hypothetical prote	platelet-derived e	calcium-dependent	hypothetical prote			probable carotenoi	probable PPE prote	hypothetical prote	hypothetical prote	stical	myelin transcripti	
QI	H86335	F96788	S48426	E96636	C72472	S25185	T13713	T10586	T02784	T39026	850565	A83042	T42207	T01236	C69494	T19543	T00974	G75627	S03904	S56652	PN0464	C70640	B75376	G75473	709	805392	T48804	T04449	T30189	
DB	7	~	7	N	7	~	7	7	Н	~	N	7	N	Н	~	~	N	N	-	Н	N	N	N	~	7	7	~	~	N	
Length	538	369	271	907	110	367	1160	257	639	172	250	467	3343	472	83	474	516	471	482	533	127	406	433	455	468	471	750	838	1182	
% Query Match	O.	œ.	15.9	ů.	5	15.1	ß	2	4	4	14.6	14.4	•	•	4	14.1	•		13.9	•	•	•	۳.	•	'n.	•	•	13.8	•	
Score	3	86.5	ω.	~	71.5	70	7	69.5	ø	۲.	٠	ė.	•	9	'n.	٠	'n.	65		64.5	64	64	64	64	64	64	64	64	64	
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2 T46637 2 T46608	2 C83263 2 T35928	E70977 T52359	: S18252 : A47062	H72237 AD2184	T02139	E83230	JC8032	T42078
F 80	9.8	90	<u>г</u> 0	9 10	23	200	00	2
118	326 468	123	370	346 445	9 2	9 7	4	52
13.8	13.7	13.7	13.7	13.6 13.6	13.6 13.6	13.6	13.5	13.5
6 4 4 4	63.5 63.5	63.5	63.5 63	99	63	63 62.5	62.5	62.5
30	332	3.5	36	38	40	42	44	4 5

ALIGNMENTS

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720H2.2 protein - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 0.2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86335
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Luu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Readiues: 1-538 <STO>
A;Cross-references: UNIPROT:Q9LNU5; GB:AE005172; NID:g8778978; PIDN:AAF79893.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Map position: 1
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Gaps <u>,</u> 29.7%; Score 137.5; DB 2; Length 538; 34.1%; Pred. No. 1.1e-06; Live 21; Mismatches 28; Indels 9; Query Match
Best Local Similarity 34.14
Matches 30; Conservative

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1 MEHYRKAGSVELP-APSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSG 59 ð 요

60 SGRAAGKAVSCAEIVKRRVPGLHQLTKL 87 ઠે 셤

protein T4012.22 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: O2-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F96788
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Nature 408, 816-820, 2000
A;Authors: Hundrer, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

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Cjaccesion: E9636
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.M.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K., ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200
A;Authors: Hunder, J., Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., J.; Jul, Y.; Liu, X.; Liu, Z.X.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Residues; 1-907 <STO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:Q9C946; GB:AE005173; NID:g6751696; PIDN:AAF27679.1; GSPDB:GN
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: C72472
R;Rawarabayasi, Y:; Hino, Y:; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
B;Rawarabayasi, Y:; Mino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
By Hes. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy.
A;Reference number: A72450; MUID:99310339; PMID:10382966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: C72472
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-110 <KAM>
A;Cross-references: UNIPROT:Q9Y965; DDBJ:AP000064; NID:g5105945; PIDN:BAA81435.1; PID:d1
A;Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 PAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAVSCAE 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein 4 - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 04-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
                             C,Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein APE2420 - Aeropyrum pernix (strain K1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.8%; Score 73; DB 2; 28.4%; Pred. No. 12;
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15.4%; Score 71.5; Di
Best Local Similarity 32.5%; Pred. No. 1.8;
Matches 25; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Conservative
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Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: T7P1.21
A;Map position: 1
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A;Gene: APE2420
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S25185
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ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A; Reference number: A86141; MUID:21016719; PMID:11130712

A; Accession: F96788

A; Accession: P96788

A; Molecule type: DNA

A; Residues: 1-369 <STO>
A; Accessive: Feferences: UNIPROT:Q9LQR7; GB:AE005173; NID:G8778814; PIDN:AAF79819.1; GSPDB:GN
C; Genetics:
A; Gene: T4012.22

A; Map position: 1
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A; Residues: 1-271 < csm.>
A; Residues: 1-271 < csm.>
A; Cross-references: UNIPROT: P41277; GB: Z47047; EMBL: Z38060; NID: g603997; PID: g763293; MI
A; Hirayama, T.; Maeda, T.; Saito, H.; Shinozaki, K.
R; Hirayama, T.; Maeda, T.; Saito, H.; Shinozaki, K.
A). Gene. 249, 127-138, 1995
A; Title: Cloning and characterization of seven cDNAs for hyperosmolarity-responsive (HORA).
A; Reference number: S63623; MUID: 96086928; PMID: 7500933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 09-Jul-2004
Accession: S48426; S63625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 HCLVFVACWEIWFRDKGSTEVVFKAMGRAINKTVTIVELIKVFFWRPALSNSRSVVQMGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ------GGSARHVVFSGSGRAAGKAVSCAEIVK--------
                                                                                                                                                                                                                                                                                                                                                                  ; Score 86.5; DB 2; Length 369;
; Pred. No. 0.17;
15; Mismatches 37; Indels 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 SGRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQ 91
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15.9%; Score 73.5; DE
Best Local Similarity 28.3%; Pred. No. 2.9;
Matches 26; Conservative 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RHR2 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YIL053w
C;Species: Saccharomyces cerevisiae
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A;Map position: 9L
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Best Local Similarity 21.4%;
Matches 28; Conservative 19
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A;Reference number: $63623; MUD:$
A;Accession: $63625
A;Wolecule type: mRNA
A;Residues: 17-266 <HIR>
A;Cross.references: EMBL:D50471
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A;Gene: SGD:RHR2
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43;

Length 907; Indels 4

Gaps

15;

Length 110; 27; Indels

DB 2;

26

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Tue Feb

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A,Gene: ATSP:F9F13.90
A,Map position: 4
C,Superfamily: proline-rich protein
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T39026
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Albescription: Dissecting the functions of beta3 of AP3 complex.
Albescription: Dissecting the functions of beta3 of AP3 complex.
Albescription: Dissecting the functions of beta3 of AP3 complex.
Albescription: Ti3713
Albescribe type: DNA
Albescribe type: DN
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10586
R;Bevan, M.; Pohl, T.; Welzenegger, T.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.; Lemcke submitted to the Protein Sequence Database, June 1999
A;Reference number: 216991
A;Accession: T10586
                   R;Dammann, T.; Wohlleben, W.
Mol. Microbiol. 6, 2267-2278, 1992
A;Title: A metalloprotease gene from Streptomyces coelicolor "Mueller" and its transcrip
A;Reference number: 825185; MUID:93023855; PMID:1406267
A;Accession: 825285
A;Status: preliminary
                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-367 <DAM>
A;Cross-references: UNIPROT:P43167; EMBL:211929; NID:g46866; PIDN:CAA77983.1; PID:g46867
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, April 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-257 <BEV>
A;Cross-references: UNIPROT:QSUNS; EMBL:AL080253; GSPDB:GN00062; ATSP:F9F13.90
A;Experimental source: cultivar Columbia; BAC clone F9F13
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 AARPQLPAP---PQLPPGLVPQLTPDRPLGRRALGLLHDLRHRAAPRRRAGTLRGLAAAL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ AL 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            betal protein - fruit fly (Drosophila melanogaster)
C,Species: Drosophila melanogaster
C,Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEHYRK---AGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 PVLDGG---HALGRGEGTVAYRCAVGHGCEDVLRHLVRRVADEGCATRPGL 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRLEGGSARHVVFSGSGRAAGKAV---SCAEIVK---RRV-----PGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGL-----
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32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 70; DB 2;
Pred. No. 9.4;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 70;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.1%;
27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 33.8%;
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCHSKDKSCREGGK 716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 15.1%
Best Local Similarity 27.9%
Matches 31; Conservative
C, Accession: S25i85; S21012
R, Dammann, T.; Wohlleben, W
Mol. Microbiol. 6, 2267-2278
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R; Zhang, Y.Q.; Broa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         703
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C;Accession: T02784

**Muxilo. I.; Jack, E.; Cordero, M.; San Segundo, B.
submitted to the EMBL Data Library, July 1998
A;Description: A calcium-dependent protein kinase possibly involved in pathogen defense
ass related RRMs gene.
A;Reference number: 214736
A;Accession: T02784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A Description: probably involved in pathogen defense in maize plants
C; Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase; cykeywords: AFP; calcium-binding; EF hand; phosphotransferase; serine/threonine-specifi:
F; 151-411/Domain: protein kinase homology «KII»
F; 159-167/Region: protein kinase AFP-binding motif
F; 454-486/Domain: calmodulin repeat homology «EFI»
F; 250-522/Domain: calmodulin repeat homology «EFI»
F; 256-558/Domain: calmodulin repeat homology «EFI»
F; 250-592/Domain: calmodulin repeat homology «EFI»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-172 <-BEV>
A;Cross.references: UNIPROT:Q10307; EMBL:Z69731; PIDN:CAA93615.1; GSPDB:GN00066; SPDB:S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein SPAC6C3.02c - fission yeast (Schizosaccharomyces pombe) C; Species: Schizosaccharomyces pombe C; Species: O3-Dec-1999 #sequence_revision O3-Dec-1999 #text_change O9-Jul-2004 C; Accession: T39026 R; Pervin, K.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, February 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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C;Species: Zea mays (maize)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 RKAGSVELPAPSPMPQLPPDTLEM------RVRDGSKIRNLLGLALGRLEGGSA
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                                                                  21;
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A;Zross-references: UNIPROT:082107; EMBL:AJ007366; PIDN:CAA07481.1
A;Experimental source: strain W64A; seed
C;Function:
Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 639;
                                                              26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33; Indele
   DB 2;
   Query Match
15.0%; Score 69.5; DE
Best Local Similarity 29.6%; Pred. No. 7.3;
Matches 24; Conservative 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 14.9%; Score 69; DB Similarity 25.6%; Pred. No. 22; 22; Conservative 15; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;182/Active site: Lys #status predicted
                                                                                                                                    20 QLPPDTLEMRVRDGSKIRNLLGLAL
                                                                                                                                                                                                                                                                                                                                     109 GRAAGRGVPTGPLVQAQ-PGL 128
                                                                                                                                                                                                                                                                      61 GRAAGKAVSCAEIVKRRVPGL 81
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A;Accession: T39026
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Best Local Similarity
Matches 22; Conserv
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64

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Dreast cancer susceptibility protein BRCA2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T42207
R;MCAllister, K.A.; Haugen-Strano, A.; Hagevik, S.; Collins, N.K.; Brownlee, H.; Futreal, submitted to the EMBL Data Library, February 1997
A;Description: Characterization of the mouse and rat homologs of the BRCA2 breast cancer A;Rcference number: Z22073
A;Accession: T42207
A;Accession: T42207
A;Accession: T42207
A;Molecule type: mRNA
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A;Cross-references: UNIPROT:035923; EMBL:U89653; NID:g2443440; PID:g2443441; PIDN:AAB713|
A;Experimental source: strain Sprague-Dawley; testes
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A;Molecule type: DNA
A;Residues: 1-472 <GEI>
A;Cross-references: UNIPROT:Q96287; EMBL:AF058919; NID:g3047100; PIDN:AAC13616.1; PID:g3
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A;Introns: 21/3; 103/3; 134/3; 154/3; 245/3; 270/3; 289/3; 336/3; 353/3; 385/3; 413/3; 4
C;Superfamily: Kinase-related transforming protein; protein kinase homology
C;Keywords: ATP; phosphotransferase; protein kinase
F;136-397/Domain: protein kinase homology «KIN»
F;144-152/Region: protein kinase ATP-binding motif
F;167/Active site: Lys #status predicted
             C,Genetics:
A,Gene: lpd3; PA4829
C,Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology
C,Keywords: redox-active disulfide
F;43-48/bisulfide bonds: redox-active #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    serine/threonine-specific protein kinase (EC 2.7.1.-) F6N23.11 [similarity] NiAlternate names: protein F6N23.11; shaggy-related protein kinase tetha C;Species: Arabidopsis thaliana (mouse-ear cress) C;Bete: 05-May-2000 #sequence_revision 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004 C;Accession: T01236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----RAA
                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                                                                                                                                                                                                                                          Length 467;
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                                                                                                                                                                                                                                                                                                                                                                            23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 PSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSG
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C;Superfamily: DNA recombination repair protein, BRCA2 type
                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rigeisel, C. submitted to the EMBL Data Library, April 1998
A; Description: The sequence of A. thaliana F6N23.
A; Reference number: Z14281
A; Accession: T01236
                                                                                                                                                                                                                                                                                 14.4%; Score 66.5; D 27.3%; Pred. No. 28; vative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 GKAVSCAEIVKRRVPGL
                                                                                                                                                                                                                                                                                                                                                                            21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
Les 18; Conserv
                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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                                                                                                                                                                                                                                                                                          Query Match
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C; Species: Saccharomyces cerevisiae
S; Soft S;
S; Spietrich, F.S.
S; Spietrich, F.S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 EHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVF--SG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 PAPSRVQQAPPPT---AVQGGSSPGFFGNLVSTAAGVGIGSAIGHTVGSVITGGFSGSG 90
                                                                                                                                                                                                                                                                                                                                                                                                            13 PAPSPMPQLPPDTLEMRVRDGSK---IRNLLGLALGRLEGGSARHVV-----FSGSG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hyperosmolarity-responsive protein HOR2 - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YER062c C;Species: Saccharomyces cerevisiae C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 09-Jul-2004 C;Accession: S50565; S63623 R;Dietrich, F.S.
                                                                                                                                                                                                                                                                                                                              13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32; Indels 21; Gaps
                                                                                                                                                                                                                                   Length 172;
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                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                               Score 67.5; DB 2;
Pred. No. 7.8;
4; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 14.6%; Score 67.5; DB Best Local Similarity 27.2%; Pred. No. 12; Matches 25; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 SGRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQ 91
A,Experimental source: strain 972h-; cosmid c6C3 C,Genetics:
A,Gene: SPDB:SPAC6C3.02c
A,Map position: 1
                                                                                                                                                                                                                               14.6%;
                                                                                                                                                                                                                      Query Match
Best Local Similarity 39.09
Matches 23, Conservative
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Conserved hypothetical protein AF1956 - Archaeoglobus fulgidus
C.Species: Archaeoglobus fulgidus
C.Species: Archaeoglobus fulgidus
C.Species: O5-Dec-1997 #sequence_revision O5-Dec-1997 #text_change 16-Aug-2004
C.Accession: C6949
R.Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, F. Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A.Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A.Ticle: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaec A. Reference number: A69250; MUID:8904933; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-89 < KLES.
A;Cross-references: UMIPROT:028323; GB:AE000968; GB:AE000782; NID:g2689291; PIDN:AAB8929 C;Superfamily: Archaeal histone-like protein, Alba type
                                                                                       3;
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                                                                                                                                                                                                             7 AGSVELPAPSPMP---QLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRA 63
Query Match
14.3%; Score 66; DB 1; Length 472;
Best Local Similarity 31.8%; Pred. No. 33;
Matches 21; Conservative 9; Mismatches 24; Indels 12; Gaps
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117 TGQVIT 122
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Search completed: January 26, 2005, 15:07:32 Job time : 19.2 secs

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Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Altachuler R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S.F., Zeeberg B. Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Aspleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergen E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Ryyminski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human

mouse CDNA sequences."
                                                                    Aas95377 desulfovi
Q94kh6 lycopersico
Q99565 aeropyrum p
Q81n54 oryza sativ
Q9564 streptomyce
Q72531 desulfovibr
Aas96284 desulfovi
                  Q9c946 arabidopsis
Q82cd4 streptomyce
Q72dn2 desulfovibr
                                                                                                                                                                                                Q6zhb3 oryza sativ
Bad07586 oryza sat
Q7vye7 bordetella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 463; DB 2; Length 163; 100.0%; Pred. No. 1e-39; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC032136; AAH32136.1; -. Genew, HGNC:19909; C9ortE730. Interpro; IRR011574; Alba DUF78. ProDom; PD010497; Alba DUF78; 1. SEQUENCÉ 163 AA; 17631 MW; 442C8727191A0BCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Chromosome 9 open reading frame 23 protein.
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                                                                                                                                                                                                                                                                                                                                                                                    163 AA
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QPP1 YEAST
Q9C946
Q9C946
Q92CD4
Q72DN2
Q9285377
Q94KH6
Q97965
Q97965
Q9781N34
Q9781N34
Q9781N34
Q72B31
Q6ZH34
Q6ZH34
Q6ZH31
AAS96284
AAS96284
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
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 Homo sapiens (Human)
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=C9orf23;
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mus musculu
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537.138 Million cell updates/sec
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                                                                                                                          January 26, 2005, 14:40:40 ; Search time 97.478 Seconds
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Q91we3
Q9bu19
Q9nx88
Q9v9b6
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                 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q6NNC7
AAR96155
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463
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BAD05714
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Q9CYX4
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Q9M8Z6
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Q7R6W6
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Q9ZPM0
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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Match Length DB
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Perfect score:
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RESULT 3
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RA Klausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Alteschul S.F., Jordan H., Moore T., Mang J., Hsieh F.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toohiyuki S., Carninci P., Prange C.,
RA Boaks S.A., McGwan P.J., McKernan K.J., Malek J.A., Mullahy S.J.,
RA Rohas S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Rohas S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
R. "Generation and initial analysis of more than 15,000 full-length human
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MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IISSUE-Mammary tumor. MMTV-LTR/INT3 model. 5 month old mouse. Taken by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNILGIALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biopsy.;

Strausberg R.;

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

R EMBL; AJ293897; CAC34588.1; --

R EMBL; BC047068; AAH47068.1; --

R EMBL; BC047068; AAH47068.1; --

R EMBL; BC047068; AAH47068.1; --

R EMBL; BC047068; AAH47069.1; --

R EMBL; BC047068; AAH47069.1; --

R EMBL; BC047068; AAH47069.1; --

R Hypothetical protein.

KW Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 163;
                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Skeletal muscle;
Ievolella C., Zara I., Lanfranchi G.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JOCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein (RIKEN cDNA 2810432D09).
Name=2810432D099Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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95.0%; Score 440; DB 2; Le
Best Local Similarity 95.6%; Pred. No. 2.4e-37;
Matches 87; Conservative 1; Mismatches 3;
                                                                        16
                                                                                                                                                                 163 AA.
                                                     MEDLINE=22388257; PubMed=12477932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA sequences."
                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=FVB/N-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=FVB/N-3;
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                                   61
                                                                                                                                                            299JH1
                                                                                                                          RESULT 2
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I will Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/6J; TISSUE=Whole body; MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Muramatsu M., Engent M., Engelected character and subtraction of cap-trapper-selected character prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810432D09 product:hypothetical protein, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-CS7BL/60; TISSUE-Whole body;
Adachi J., Azawa K., Akahira S., Akimura T., Arai A., Aono H.,
Azakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/64; TISSUE=Whole body;
MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Kiisunani T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yujiwanoto R., Matumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwa S., Ishikawa T., Ozawa K., Tanaka T., Matumra S., Kawai J., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matumra S., Kawai J., Rikiki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAINE-STYBL/66; TISSUE-Whole body;
MEDILINE-21085660; Pubmed-11217851;
RIKEN FANYOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Whole body;
MEDLINE-99279253; Pubmed-10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                          163 AA.
5
                                                                        91
                                                61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQ
                                                                                                                                                                                                                                                                                                                                                   Created)
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                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insert sequence.
Name=2810432D09Rik;
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57.1%; Score 264.5; DB 2
48.1%; Pred. No. 4.3e-19;
iive 17; Mismatches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99279253; PubMed=10349636;
                                              52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA sequences.
                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                     Ouery Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                           Name=Rpp25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                  9
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"Generation and initial analysis of more than 15,000 full-length human
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Subaitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO13222, BAB28723.1, -.
                                                                                                                                                                                                                                                                                                1 MEQYREAGSVELPASSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSTRHVVFSGS
                                                                                                                                                                                                                                                                                 1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi, Cypriniformes;
                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                         2; Length 163;
                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC076268; AAH76268.1; -.
Hypothetical protein:
SEQUENCE 224 AA; 24369 MW; C2FD38C9D8B2F38A CRC64;
                                                                                                                                                                             Hypothetical protein. -
SEQUENCE 163 AA; 17648 MW; DC89421F4F617429 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2004 (TrEMBLrel. 28, Created)
01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                       Score 439; DB 2;
Pred. No. 3e-37;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                        GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                              224 AA
                                                                                                                                                                                                                                                                                                                                                                     GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQ 91
                                                                                                                                             InterPro; IPR011574; Alba DUF78.
                                                                                                                                                                                                                       94.8%;
                                                                                                                                                                                                                                  Local Similaricy
nes 87; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyprinidae; Danio.
NCBI TaxID=7955;
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Straubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Altauener R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altachul S.P., Zeeberg B. Buetow K.H., Schaefer C.F., Baher N.K.,
Altachul S.P., Jozdan H., Moore T., Max S.I., Wang J., Haich F.,
Angeleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                      1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSA----- 52
                                                                                                                                                                                                                                                       1 MENYRKANTIEQPCPCPPPDLPSDTPEVRVKDGSKIRNLMRFALSRMEBETAASADHEGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Ribonuclease P 25kDa subunit (Mus musculus ES cells cDNA, RIKEN full-
length enriched library, clone:C330033C13 product:hypothetical
protein, full insert sequence).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalja, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                     19;
                                                                                                                                                                                                                                                                                                                                                                                              61 EVSVGTGDNLCRQIVFTGVGGSVAKAITCVEIMKRRIHGLHQLTKLAY 108
    Length 224;
                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                     Indels
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                     20;
DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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TISSUENCE FROM N.A.

TISSUESERAID, and Skin;

RA STRAUBBERS R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

RA Altachul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,

Altechul S.F., Zeeberg B. Buecow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Rapleron M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robak S.A., McEwan P.-J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Robak S.A., McEwan P.-J., Wakan S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

Rabay J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Garimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rabak S.A., Marra M.J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=21998191; PubMed=12003489;
Guerrier-Takada C., Eder P.S., Gopalan V., Altman S.;
"Purification and characterization of Rpp25, an RNA-binding protein subunit of human ribonuclease P.";
                                                                    Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
          protein (RNase P protein subunit p25)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY034074; AAK54443.1; -. IntAct; Q9BUL9; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; BC002497; AAH02497.1; -. EMBL; BC007270; AAH07270.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9NX88
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Q9NX88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEHYRKAGSVELPA-----PSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MENFRKVRSBEAPAGDGDEGGSPNSGPFADLAPGAVHMRVKEGSKIRNLLAFATASMAQP 60
                                   The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; Analysis Genome Exploration Research Group Phase I & II Team; Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                       MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata X., Itoh M., Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Nuramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA lbraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE_20530913; PubMed=11076861; Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RIKIN integrated sequence analysis (RISA) system 384-format genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l protein. -
199 AA; 21037 MW; B9DE105BE3293D64 CRC64;
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Last sequence update)
Last annotation update)
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    48.4%; Score 224; DB 2; L/
1 Similarity 47.5%; Pred. No. 5.7e-15;
47; Conservative 14; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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ProDom; PD010497; Alba DUF78; 1.
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SEQUENCE FROM N.A.
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Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                     STRAIN=C57BL/6J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Q9BUL9
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                                                                                                                                   1 MEHYRKAGSVELPA-----PSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGG
                                                                                                                                                            Gaps
                                                                                                28; Indels 10;
                                                      Query Match 47.9%; Score 222; DB 2; Length 199; Sest Local Similarity 46.5%; Pred. No. 9.1e-15; Atches 46; Conservative 15; Mismatches 28; Indels
ProDom; PD010497; Alba_DUF78; 1.
SEQUENCE 199 AA; 20632 MW; 9A4494F0297B2A81 CRC64;
                                                                                                                                                                                                            51 SARHVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRF 89
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Lewis S.E.;
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                                                                                                                                                                                                                                                                                                                                                                                              1 MEHYRKAGSVELPA-----PSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGG 50
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                                                                                                                                                                                                                                                                                                                    47.1%; Score 218; DB 2; Length 199;
45.5%; Pred. No. 2.4e-14;
ive 15; Mismatches 29; Indels 10; Gaps
                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                        Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO00381; BAA91128.1; -.

InterPro; IRROII574; Alba DUF78.

PRODOM; PO10497; Alba DUF78.

PRODOM; PO10497; Alba DUF78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
                                                                                                                                                                                                                                                                                   199 AA; 20660 MW; 855494F0366B2291 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 SARHVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRF
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NCBI_TaxID=7227;
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                                  Hypothetical protein FLJ20374.
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                                                                                                                                                                                                                                                                                                                                                         45; Conservative
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Best Local Similarity
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                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                   NCBI_TaxID=9606;
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Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Shenert K., Remington K., Saunders R.D., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T., Sylisks R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Weinstock G.M., Weissenbach J., Weinstock G.M., Weissenbach J., Xen R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhong F.N., Zhong W., Zhuo W., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Fries E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MEHYRKAGSVE-----LPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE-2242065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., Patel S., Adams R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
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MEDLINE-22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Mallburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 287:2185-2195(2000).
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IntAct; Q9V9B6; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomics perspective.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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SEQUENCE FROM N.A.
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                                                                                                     RE65722p.
                                                AAR96155
AAR96155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                          65
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                                                                                                                                                                                                                                                                                                                                              1 MEHYRKAGSVE-----LPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSAR
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                              Anopheles gambiae str. PEST.
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Berkeley,
Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BT011363; AAR96155.1; -
SEQUENCE 206 AA; 23162 MW; 8B9FD01C279BC5D9 CRC64;
                                                                                                                                                                          Anopheles Genome Sequencing Consortium;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                         Length 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 206;
                                                                                                                                                                                                                                                                                                               Indels
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215 AA; 24004 MW; AA72B25FAA8ABFBE CRC64;
                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                      Query Match 35.9%; Score 166; DB 2; Lv
Best Local Similarity 43.3%; Pred. No. 5.9e-09;
Matches 39; Conservative 16; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CVVWSGSGGGVVKTICCAEVLKRSHP-LYQVTRMAY 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54 HVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRF 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.0%; Score 162; DB 2;
40.6%; Pred. No. 1.5e-08;
iive 16; Mismatches 33
                        215 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 AA
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                                                                                                                                                                                                                                                                                                                                                                                            Created)
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                                                                                                                                                                                                                     preliminary data.
EMBL; AAAB01008807; EAA03913.2; -.
                                                                         ENSANGP0000016002 (Fragment)
Name=ENSANGG0000013513;
                                         01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                  NCBI TaxID=180454;
                                                                                                                                                     SEQUENCE FROM N.A.
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Name=CG9422;
                                          01-MAR-2004
01-MAR-2004
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NON TER
SEQUENCE
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                    Q7PTH5
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Matches
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MMHYRKAENVEKELSKSDLPFEDCMPKSQKDFLWMHVKGGTKVSNVIEFAQEALNKGEHR
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Ar1920220/120H2.3.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     George R., Pacleb J.,
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Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
Banh J., Bawser L., Carninci P., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
HSSP: O28323: INFJ.
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                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Bphydroidea; Drosophilidae; Drosophila.
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Stapleton M., Carlson J., Chavez C., Frise E., George R. Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, BT011363; AAR96155.1;
SEQUENCE 206 AA, 23162 MW; 8B9FD01C279BC5D9 CRC64;
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                                                                                    Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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29.7%; Score 137.5; DB 2;
Local Similarity 34.1%; Pred. No. 7.7e-06;
les 30; Conservative 21; Mismatches 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.0%; Score 162; DB 2; 40.6%; Pred. No. 1.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54 HVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRF
206 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 AA
                                                      Created)
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                                                02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.61
Matches 39; Conservative
PRELIMINARY;
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Local Similarity 32.23
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                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Devoler R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J., Cheuk R., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
Sakano H., Vaysberg M., Lee J.M., Lenz C., Liu S., Pham P., Toriumi M., Yu G., Chin C., Chiou J., Choi E., Chung M., Gonzalez A., Howng B., Liu A., Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.; Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AC022472, AR778893.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Arabidopsis thallana (Mouse-ear cress).
Bukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            538 AA; 58572 MW; 1B0BB141F0F9AF22 CRC64;
                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                       SGRAAGKAVSCAEIVKRRVPGLHQLTKL
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ProDom; PD010497; Alba DU\overline{F}78; 1.
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Matches 30; Conservative
                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                             Name=T20H2.2;
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Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas B., Wu D.,
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Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Tang C.C., Tortumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
Shinozaki K., Danis R.W., Theologis A., Ecker J.R.,
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                        Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.K., Jones T., Kaniya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
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Ecker J.R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
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ProDom; PD010497; Alba DUF78; 1.
SEQUENCE 350 AA; 37383 MW; DB474865DF4E162E CRC64;
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EMBL; AY054208; AAL06669.1; --
EMBL; AF412102; AAL06555.1; --
EMBL; AY124847; AAM70556.1; --
HSSP; P74761; 1HOX.
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01-0TT-2000 (TrEMBLrel. 15,
01-0TUN-2003 (TrEMBLrel. 24,
F17A9.19 protein.
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RA Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.

BEMBL; ACO16827; AAF27007.1; -.

DR HSSP; P74761; 1HOX.

Query Match

Query Match

27.1%; Score 125.5; DB 2; Length 485;
Beet Local Similarity 31.3%; Pred. No. 0.0021;
Matches 26; Conservative 17; Mismatches 33; Indels 7; Gaps 1;

QY I MEHYKAGSVELPAPSPMQLPPTLEMFVDGSKIRNLGLALGELEGGSARHVVFSGS 60

| HSSP; P74761; HSSP; P74761; HSSP 1; H
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Search completed: January 26, 2005, 15:06:27 Job time : 99.478 secs

61 GRAAGKAVSCAEIVKRRVPGLHQ 83 |:| | |: | |: | | || | 54 GQAISKTVAISEILKNKIPGLHQ 76

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Abo69785 BAbg23459 BAdj70368 BAgg48477

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The invention relates to full length GENSET human nucleic acids encoding potentially secreted proceins. The nucleic acids and the polypeptides they encode may be used in the prevention, treatment and disgnosis of diseases associated with inappropriate GENSET gene expression. For gene expression by rectifying mutations or deletions in a patient genome that affect the activity of GENSET or by supplementing the patients own production of GENSET polypeptides. Conversely, antisense expression by binding with the cells' own genes and preventing their expression by binding with the cells' own genes and preventing their expression. The sense and antisense nucleic acids may also be used as DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; secreted protein; gene therapy; vaccine; treatment; diagnosis; GENSET.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Full length GENSET human nucleic acids encoding potentially secreted proteins, useful in gene therapy and vaccination against a variety of diseases, and for diagnosis of those diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bougueleret L, Jobert S;
                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein, SEQ ID NO: 459
                                           ABO65891
ABP62768
ABJ627768
ABJ60334
ABW57277
AAW30633
AAW30623
AAY26169
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AAY4836
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06-MAR-2000; 2000US-0187470P
 Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-367870/38.
N-PSDB; AAH64942.
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1 MEHYRKAGSVELPADSPMPQ......EIVKRRVPGLHQLTKLRFLQ
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              GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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AAG33137

Zea mays Zea mays

Aag34072 Aag34071 Aag33137

Aag33136

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probes in diagnostic assays to detect and quantitate the presence of shiltar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to expression and antigorists and antagonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET polypeptide the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human polynucleotides and the polypeptides they encode. The polynucleotides and polypeptides are useful in diagnostics, corensics, gene mapping, medical imaging, identification of mutations responsible for genetic disorders or other traits, assessing biodiversity and producing many other types of data and products dependent on DNA and amino acid sequences. They are also useful for preventing, treating or ameliorating medical conditions, such as cancer, neurodegenerative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; genetic disorder; gene mapping; medical imaging; cancer; neurodegenerative disorder; lymphoid cell disorder; osteoporosis; Parkinson's disease; Alzheimer's disease; bone degenerative disorder; osteoarthritis; periodontal disease; liver fibrosis; viral infection; fungal infection; autoimmune disease; diabetes;
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                                                                                                                                                                           Length 163;
                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Goodrich R, Asundi V, Zhang J, Zha
la Y, Yamazaki V, Chen R, Wang Z,
Wang D, Drmanac RT;
                                                                                                                                                                    100.0%; Score 463; DB 4;
100.0%; Pred. No. 7.6e-47;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                    GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQ 91
                                                                                                                                                                                                                                                                                                                           Claim 9; SEQ ID NO 633; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                        ABU00014 standard; protein; 163 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human novel polypeptide #107.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAR-2002; 2002WO-US005109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAR-2001; 2001US-00810173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                       91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhou P, Go
Yang Y, Ma
T, Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2003-040556/03
                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                atopic dermatitis
                                                                                                                                      Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABX05092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200274961-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABU00014;
                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
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 88888888888
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disorders (e.g. Parkinson's disease, Alzheimer's disease), lymphoid cell disorders, osteoporosis, osteoarthritis, bone degenerative disorders, periodontal disease, liver fibrosis, infections (e.g. viral, fungal or bacterial) or autoimmune diseases (e.g. diabetes, atopic dermatitis). Sequences ABG99888-ABG9989 and ABU00010-ABU00433 represent human polypeptides of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied by the European Patent Office
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiovascular disorder; isobaemic heart disease; asthma; cardiovascular disorder; isobaemic heart disease; asthma; pneumonia; acute myocardial infarction; respiratory disease; asthma; pneumonia; cystic fibrosis; chronic renal failure; glomerulopathy; gastrointestinal disorder; peptic ulcer; cirrhosis; immune disorder; HIV infection; systemic lupus erythematosus; endocrine system; diabetes mellitus; epilepsy; Alzheimer's disease; amyotropic lateral sclerosis; skin disorder; psoriasis; bacterial; thrombolytic; antianaemic; cardiant; vasotropic; antiasthmatic; antianaemic; cardiant; vasotropic; antiasthmatic; antialeramatory; nephrotropic; antiulcer; hepatotropic; immunosuppressive; antialeralic; dermatological; antirheumatic; antidiabetic; anticonvulsant; neuroprotective; nootropic; antipacriatic; antibacterial; fungicide; antiparasitic; virucidal;
                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                 1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                                                         1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLGGSARHVVFSGS
                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                 Length 163;
                                                                                                                                                                                                                                  Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human; cancer; haematopolesis; thrombosis; anaemia;
                                                                                                                                                                                            100.0%; Score 463; DB 6;
100.0%; Pred. No. 7.6e-47;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human pharmaceutically useful protein SegID 381.
                                                                                                                                                                                                                                                                                                                                       91
                                                                                                                                                                                                                                                                                                                                                             61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQ 91
                                                                                                                                                                                                                                                                                                                                   61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADM90988 standard; protein; 219 AA
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2002US-0406640P.
2002US-0406655P.
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2002US-0410946P.
2002US-0410951P.
2002US-0410953P.
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2002US-0410960P.
2002US-0410962P.
2002US-0411019P.
2002US-0411022P.
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2002US-0406612P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-2004 (first entry)
                                                                                                                                                                                                                             91; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy; vaccine
                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                           Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004020595-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2002;
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29-AUG-2002;
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                                                                                                                                                                                                                           Matches
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 8888888888888
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This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a wartety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopoiesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to identify individuals to the extended cDNAs. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases
                            Secreted protein; human; cytokine; cellular proliferation; cell movement; cellular differentiation; immune system regulator; anti-inflammatory; haematopoiesis regulator; tissue growth regulator; tumour inhibitor; reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy; genetic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 163;
      Extended human secreted protein sequence, SEQ ID NO. 489.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 457; DB 2;
Pred. No. 3.9e-46;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GRAAGKAVSCAEIVKRRVPGLHQLTKLXFLQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; genetic disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 9; Page 423-424; 516pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated human secreted proteins.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human secreted polypeptide #263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADP19412 standard; protein; 163
                                                                                                                                                                                                                                                                                                                                      97US-0069957P.
98US-0074121P.
98US-0081563P.
98US-0096116P.
                                                                                                                                                                                                                                                                                                   98WO-IB002122
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98.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-385906/32.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bougueleret L,
                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                                                                              W09931236-A2
                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                               17-DEC-1998;
                                                                                                                                                                                                                                                                                                                                        17-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to novel isolated human polynucleotides and the encoded proteins thereof. Specifically, it refers to proteases, kinases, phosphatases, secreted and transmembrane proteins, as well as the derived complete fragments, which can be used to develop antibodies and screen for peptide fragments, which can be used to develop antibodies and screen for comall molecule agonists and antagonists that can modulate their activities. The present invention describes polypeptides, preventing activities. The present invention describes polypeptides, preventing and treating proliferative disorders, e.g. cancer, disorders of and treating proliferative disorders, e.g. cancer, disorders of haematopoiesis such as thrombosis and anaemia, cardiovascular disorders, e.g. is asthma, pneumonia or cystic fibrosis, disorders of the kidney and urinary tract, e.g. chromic renal failure and glomerulopathy, diseases, e.g. HIV infection and system clupus erythematicsus, disorders of the endocrine system, e.g. diabetes mellitus, central nervous system disorders, e.g. epilepsy, altheimer's disease or amyotropic lateral contingential disorders, e.g. psoriasis, they exhibit many various conting in antibuding cytostatic, anticoagulant, thrombolytic anticoagulant, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antianaemic, cardiant, vasotropic, antiasthmatic, antiinflammatory, nephrotropic, antiulcer, hepatotropic, immunosuppressive, antiallergic, dermatological, antirheumatic, antiarthritic, antidiabetic, anticonvulsant, neuroprotective, nootropic, antipsoriatic, antibacterial, fungicide, antiparastic and virucidal, such that these polymucleotides can be used for gene therapy purposes and the development of appropriate vaccines. This polypeptide is a human protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                    New human polynucleotides and polypeptides, useful for diagnosing, preventing and treating proliferative disorders, immune disorders, cardiovascular disorders, or bacterial, fungal, parasitic and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 463; DB 8; 100.0%; Pred. No. 1.1e-46;
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                                                                                                                                                                       PHYSICAL & CHEM RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 381; 254pp; English.
                                                                                                                                                                                                                                    Hestir
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                                                                                                                                             PRIME THERAPEUTICS
                                       2002US-0411046P.
2002US-0411052P.
2002US-0411082P.
                                                                                                                                                                                                                                  Lee E,
                                                                                                      2002US-0411111P
                                                                                                                                                                                                                                                                                             N-PSDB; ADM90779, ADM91197.
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                                                                                                                                                                                                                                  Chu K,
                                                                                                                                                                                                                                                                         2004-257410/24
                                                                                                                                                                                        DNAFORM KK.
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                                                                                                                                             FIVE PRIKEN
                     17-SEP-2002;
17-SEP-2002;
17-SEP-2002;
                                                                                                                                                                                                                             Williams LT,
                                                                                17-SEP-2002;
17-SEP-2002;
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                                                                                                                                               (FIVE-)
                                                                                                                                                                                        (DNAF-)
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2XXXEX
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human secreted proteins expressed sequence tags (ESTs) for human secreted proteins expressed in prostate, and encode the proteins contains a secreted proteins expressed in prostate, and encode the proteins given in AAY11716 to AAY11931 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The products of a secreted human gene concleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation and differentiation activity, hemmatopies regulating activity, tissue growth regulating activity, reproductive hormone regulating activity, receptor/ligand activity, anti-inflammatory continuous inhibition activity, and chromosome mapping procedures.

The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acidic encoding the signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell
          reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
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100.0%; Pred. No. 5.9e-40;
Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Lacroix B;
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                                                                                                                                                                                                                                                                                                                                                                                                 Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 34; Page 648; 675pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG03599 standard; protein; 78 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRAAGKAVSCAEIVKRRVP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GRAAGKAVSCAEIVKRRVP 79
                                                                                                                                                                                                                                          98WO-IB001232
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Best Local Similarity 100.
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                              Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-153780/13.
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                                                                                                                                                                                                                                                                                                                                              (GEST ) GENSET
                                                                                                                                                                                                                                                                                          01-AUG-1997;
                                                                                      Homo sapiens
                                                                                                                                                                                       11-FEB-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG03599;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ద
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The sequence data for this patent did not form part of the printed plant and plant was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated polynucleotide encoding secreted polypeptide, useful for gene therapy, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, secreted protein; EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cytokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                         Bougueleret L, Jobert S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human 5' EST secreted protein SEQ ID No: 550.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; SEQ ID NO 668; 113pp; English.
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                                                                                                                                                                                                                       09-FEB-1999; 99WO-IB000282.
21-JUN-2000; 2000WO-IB000951.
15-SEP-2000; 2000US-00663600.
                                                                                                                                                 15-OCT-2001; 2001US-00978360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-440404/41.
N-PSDB; ADP19007.
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                                             US2004110939-A1.
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Homo sapiens.
                                                                                                10-JUN-2004
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Length 79;

Wang D; Zhao QA;

Ren F, War Zhang J,

Qian XB, Yang Y,

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The invention relates to human nucleic acids (AAIS7798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppeassant and cyrostatic activity. The polymucleotides are useful in gene therapy. A composation containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous is system, such as peripheral nervous system diseases, such as localised neuropathies and central nervous system disease, such as alzehier's, Parkinson's disease, Huntingron's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the activities such as: Immune system suppression, activity, chemotectic/chemokinetic activity, chemotectic/chemokinetic activity, haemostatic and thrombolytic activity, architits and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MEHYRKAGSVEL-----PAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 MENFRKVRSEEAPRGCGAEGGGPGSGPFADLAPGAVHMRVKEGSKIRNLMAFATASMAQP 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster polypeptide SEQ ID NO 20022.
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45.5%; Pred. No. 1.7e-17;
iive 15; Mismatches 29;
                                                                                                                                                                                                                                                                        Tang YT, Liu C, Agundi V, Chen R, Ma Y, (Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 2118; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB64410 standard; protein; 205 AA.
                                                                     21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-00598042.
                                                                                                                                            03-AUG-2000; 2000US-00653450
14-SEP-2000; 2000US-00662191
19-OCT-2000; 2000US-00693036
                    26-DEC-2000; 2000WO-US034263
                                                                                                                           19-JUL-2000; 2000US-00620312
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                                                                                                                                                                                                                                                                                                                                                WPI; 2001-442253/47.
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Best Local Similarity
                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                   29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
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                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
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                                                                                                                                                                                                                                                                                                                                                               Claim 13; SEQ ID NO 7680; 71pp + Sequence Listing; English
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Pred. No. 4e-39;
0; Mismatches 0; Indels
                                                                                                                                                                                                   Duclert A, Giordano J;
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100.0%; Pred. No....
0; Mismatches
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                                                                                      21-FEB-2000; 2000EP-00200610
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Best Local Similarity
Matches 78; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 78 AA;
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                                                                                                                                                             (GEST ) GENSET
                                                                                                                           26-FEB-1999;
                  EP1033401-A2
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                                                    06-SEP-2000.
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AAM38973
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Length 211; 29; Indels

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99US-0126462P.
99US-0127462P.
99US-0128714P.
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99US-0130449P.
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99US-0134221P.
99US-0134370P.
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990S-0139462P

990S-0139463P

990S-0139763P

990S-01403817P

990S-0140381P

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99US-0137222P.
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9905-0137724P
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99US-0142977P.
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06-APR-1999;
08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
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19-MAY-1999;
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24-MAY-1999,
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     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), processed DNA ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                            3 HYRKAGSVE-----LPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHV 55
                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridieation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                            8; Gaps
                                                                                                                                                                                                          Disclosure, SEQ ID NO 20022; 21pp + Sequence Listing, English.
                                                                                                                                                                                                                                                                                                                                                                    Match 35.4%; Score 164; DB 4; Length 205; Local Similarity 41.5%; Pred. No. 4.5e-11; les 39; Conservative 16; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana protein fragment SEQ ID NO: 45394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRF 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li PWD, Myers EW;
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99US-0123180P.
99US-0123548P.
                                                             23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                        23-MAR-2001; 2001WO-US009231
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                                                                                                                Venter JC, Adams M,
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                                                                                           (PEKE ) PE CORP NY.
                                                                                                                                               N-PSDB; ABL08513
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 WO200171042-A2
                                                                                                                                                                                        interactions.
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05-MAR-1999;
09-MAR-1999;
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                     27-SEP-2001
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R 16-UUL-1999; 99US-0144085P.
RR 19-UUL-1999; 99US-0144085P.
RR 19-UUL-1999; 99US-0144328P.
RR 19-UUL-1999; 99US-0144331P.
RR 19-UUL-1999; 99US-0144331P.
RR 19-UUL-1999; 99US-0144331P.
RR 20-UUL-1999; 99US-0144331P.
RR 21-UUL-1999; 99US-0144331P.
RR 22-UUL-1999; 99US-014508P.
RR 22-UUL-1999; 99US-014308P.
RR 22-UUL-1999; 99US-011308P.
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RR 23-REP-1999; 99US-01
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                    Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana protein fragment SEQ ID NO: 17635.
                                                                                                                                                                                                                                                                                                                                                                                         60 SGRAAGKAVSCAEIVKRRVPGLHQLTKL 87
                                                                                                                                                                                                                                                                                                                                                                                                    AAG16838 standard; protein; 350 AA
         990S-015832P

990S-015833P

990S-0159294P

990S-0159294P

990S-0159331P

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990S-0159631P

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990S-0160741P

990S-016077P

990S-016077P
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990S-0161359P.
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08-0CT-1999;
13-0CT-1999;
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26-0CT-1999;
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05-MAR-1999;
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25-MAR-1999;
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99US-0142920P.
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09-JUL-1999
   MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS 60
                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                          27.8%; Score 128.5; DB 3; Length 350; 32.2%; Pred. No. 1.4e-06; ive 15; Mismatches 37; Indels 7
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99US-0123180P.
99US-012548P.
99US-0126264P.
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99US-0126785P.
9905-0159293P.
9905-0159294P.
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9905-0159330P.
9905-0159633P.
9905-0159638P.
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9905-0161761P.
9905-0161761P.
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es 28; Conserv
13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
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05-MAR-1999;
03-MAR-1999;
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25-MAR-1999;
01-ARR-1999;
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PR 19-UUL-1999; 99US-0144334P.
PR 20-UUL-1999; 99US-0144332P.
PR 20-UUL-1999; 99US-0144632P.
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PR 13-CCT-1999; 99US-015329P.
PR 13-CCT-1999; 99US-015329P.
PR 13-CCT-1999; 99US-015323P.
PR 13-CC
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                                                                                                                                                                                                                                                                                              1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                         27.8%; Score 128.5; DB 3; Length 350; 32.2%; Pred. No. 1.4e-06; tive 15; Mismatches 37; Indels 7
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                                                                                                                                                                                                                                                                                                                                    61 GRAAGKAVSCAEIVKRRVPGLHQLTKL 87
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99US-0159329P
99US-01593310P
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99US-016196P
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990S-0125548P.
990S-0126264P.
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990S-012874P.
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Best Local Similarity 32.2%
Matches 28; Conservative
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        14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
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22-0CT-1999;
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
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16-APR-1999;
16-APR-1999;
116-APR-1999;
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This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up characteristics. Specifically, it refers to identifying genes that are up can regulated in transgenic plants overexpressing the heterodimeric STRAJDPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes consymmes, therapeutics, plants for the production of growth regulators, chrzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal cransduction, storage lipid mobilisation and/or altered photosynthesis, cach relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell cranscription factors. This polypeptide sequence is thate cress protein expressed by a gene upregulated 1.3 fold or more in plants overexpressing conversing the EzganDpa transcription factor, given in an exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Altering plant characteristics, useful for producing plants for enzyme c
pharmaceutical production comprises modifying in a plant, expression of
one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 78.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27.8%; Score 128.5; DB 8; Length 350; 32.2%; Pred. No. 1.4e-06; ive 15; Mismatches 37; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GRAAGKAVSCAEIVKRRVPGLHQLTKL 87
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Best Local Similarity 32.2%
Matches 28; Conservative
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N-PSDB; ADN72182.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 778.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plant, transgenic, E2Fa/DPa transcription factor; growth regulator; animal feed product; thale cress; cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27.8%; Score 128.5; DB 3; Length 350; 32.2%; Pred. No. 1.4e-06; Ative 15; Mismatches 37; Indels 7.
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990S-0160814P.
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N-PSDB; ADN72882.
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셤 8 유

Claim 1; SEQ ID NO 78; 134pp; English.

This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up characteristics. Specifically, it refers to identifying genes that are up CC - or down-regulated in transgenic plants overexpressing the heterodimeric EZRa/DPa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes companies, theraspeutics, pharmaceuticals and animal feed products, where can suppose the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal cransduction, storage lipid mobilisation and/or altered photosynthesis, cach relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell corresponding and/or carbon metabolism or they function as transcription factors. This polypeptide sequence is thale cress protein carbon and contaction of the EZFa/DPa transcription factor, given in an exemplification of the invention.

Sequence 350 AA;

Gaps 7; Query Match 27.8%; Score 128.5; DB 8; Length 350; Best Local Similarity 32.2%; Pred. No. 1.4e-06; Matches 28; Conservative 15; Mismatches 37; Indels 7; 1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS 60

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61 GRAAGKAVSCAEIVKRRVPGLHQLTKL 87

Search completed: January 26, 2005, 15:01:05 Job time : 92.6915 secs

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January 26, 2005, 15:06:38; Search time 75.8847 Seconds (without alignments) 433.254 Million cell updates/sec
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1 MEHYRKAGSVELPAPSPMPQ......EIVKRRVPGLHQLTKLRFLQ 91
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

_	459, App 459, App 668, App 668, App 227821, 109378, 221292, 224668, 229595, 1182741, 1182741,	
Description	Sequence 459, Sequence 459, Sequence 2373 Sequence 2378 Sequence 1093 Sequence 1256 Sequence 2546 Sequence 2546 Sequence 1527 Sequence 1527 Sequence 1527 Sequence 1627	•
SUMMARIES	US-09-731-872-459 US-09-731-872-459 US-09-876-997-459 US-10-425-115-237341 US-10-424-599-237821 US-10-427-963-109378 US-10-437-963-156973 US-10-425-115-231292 US-10-427-963-156973 US-10-427-963-156973 US-10-437-963-156741 US-10-437-963-184232 US-10-437-963-184322	
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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwai
TITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 237341
LENGTH: 72
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Remaining Prior Application data removed - See File Wrapper or PALM,
NUMBER OF SEQ ID NOS: 810
SOFTWARE: Patent.pm
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Pred. No. 1.9e-42;
0; Mismatches 1;
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US-10-425-115-237341
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98.7%;
                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: misc_feature
; LOCATION: (36, 47, 54, 65,
; OTHER INFORMATION: unknown
US-09-978-360A-668
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.94
Matches 90, Conservative
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ORGANISM: Homo sapiens
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                                                                                                         GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Dumas Milne Edwards, Jean Baptiste
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US4.CIP
CURRENT APPLICATION NUMBER: US 69/731,872
FRIOR FILING DATE: 2000-12-07
FRIOR FILING DATE: 2000-03-06
FRIOR FILING DATE: 2000-03-06
FRIOR FILING DATE: 1999-12-08
FRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SOFTWARE: Patent.pm
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 668, Application US/09978360A

Publication No. US20040110939A1

GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste Dumas Milne
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
APPLICATION NUMBER: US/09/978,360A
CURRENT FILING DATE: 1997-11-13
FRIOR FILING DATE: 1997-11-13
FRIOR PLING DATE: 1998-02-09
FRIOR PLING DATE: 1998-04-13
FRIOR PLING DATE: 1998-04-13
FRIOR FILING DATE: 1998-04-13
FRIOR FILING DATE: 1998-08-10
FRIOR FILING DATE: 1998-11-13
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100.0%; Score 463; DB 10; Length 163;
Best Local Similarity 100.0%; Pred. No. 4e-43;
Matches 91; Conservative 0; Mismatches 0; Indels 0.
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                                                                 Application US/09876997
o. US20030152921A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-997-459
                                                                    Sequence 459, Ap
Publication No.
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APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Cao, Yongwei APPLICANT: Wu, Wei APPLICANT: Wu, Wei APPLICANT: Buckharov, Andrey A. APPLICANT: Barbazuk, Brad APPLICANT: Li, Ping TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
                                                                                                                                                                             APPLICANT: La Royalic, David K.
APPLICANT: Sovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants
FILE REPERENCE: 38-21 [53222] B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 231292
LENGTH: 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match

26.6%; Score 123; DB 17; Length 359;
Best Local Similarity 34.1%; Pred. No. 4.5e-05;
Matches 29; Conservative 16; Mismatches 34; Indels 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: PAT_MRT4530_5658C.1.pep
US-10-437-963-156973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_142534C.1.pep
US-10-425-115-231292
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OTHER INFORMATION: ungure at all Xaa locations
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
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Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
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; Sequence 109378, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wai
; APPLICANT: Wu, Wai
; APPLICANT: Wu, Wai
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT FILLING NUMBER: US/10/437,963
; CURRENT FILLING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 109378
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (33.22) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 237821
TYPE. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26.8%; Score 124; DB 16; Length 671; 34.1%; Pred. No. 7.3e-05;
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431 AISKSVAVAEIIKKRVPGLYQDTNI 455
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; Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 34.19
Matches 29; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
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GRAINKTVMIAELIKRRIVGLHONT

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APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

BEDITH: 261

TURNING APPLICATION WITH APPLICATION PROPERTY

THE REPRESENCE: 2003-05-14

TURNING DATE: 2003-05-14

TURNING DATE: 204966
                                                                                                                                                                                                                                                                                                                                                                                                                                  ...erlCANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 152741

LENGTH: 263

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT4530_52762C.1.pep
US-10-437-963-152741
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LOCATION: (1)..(261)
OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.
                                                  54 GRAINKTVMIAELIKRRIVGLHONTOI 80
61 GRAAGKAVSCAEIVKRRVPGLHQLTKL 87
                                                                                                                                                                                                                                                                          Sequence 152741, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Xovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Wei
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Best Local Similarity 29.4%
Matches 25; Conservative
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                            US-10-437-963-152741
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US-10-437-963-184232
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                                                                                                                                                                                                                                                    APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thoma APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Con. Youngwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FITLE OF INVENTION: Plants
FILE BEFERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NO 254668
LENGTH: 242
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; Bedication No. US20040031072A1
; GENERAL INFORMATION:
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: La Coa Yongway
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Asset TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Soy Nucleic Acid Molecules Asset ILE REFERENCE: 38-21(53223) B
; CURRENT APPLICATION NUMBER: US/10/424, 599
; CURRENT FILING DATE: 2003-04-28
; SEQ ID NO 225955
; LENGTH: 245
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25.4%; Score 117.5; DB 17; Length 242;
Best Local Similarity 31.0%; Pred. No. 0.00011;
Matches 27; Conservative 14; Mismatches 39; Indels 7;
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US-10-424-599-229595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: MRT4577_163838C.1.pep
US-10-425-115-254668
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OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                           Sequence 254668, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
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ORGANISM: Zea mays
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US-10-424-599-229595
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Query Match 25.1%
Best Local Similarity 40.7%
Matches 24; Conservative
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ORGANISM: Zea mays
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LENGTH: 178
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| Sequence 60641, Application US/10425114
| Publication No. US20040034888A1
| GENERAL INFORMATION:
| APPLICANT: Liu, Jingdong
| APPLICANT: Chu, Yinda
| APPLICANT: Screen, Steven E
| APPLICANT: Goo, Yongwei
| TITLE OF INVENTION: Mucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TITLE OF INVENTION: Nucleic Acid Molecules Thereof for Plant Improvement
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
| TURENT APPLICATION NUMBER: US/10/425,114
| CURRENT APPLICATION NUMBER: US/10/425,114
| UNUMBER OF SEQ ID NOS: 73128
| SEQ ID NO 60641
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 201476, Application US/10425115

Publication No. US20040214272A1

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: APPLICANT: Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: VS/105222) B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT PILING DATE: 2003-04-28
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                                                                                          Query Match 25.1%; Score 116; DB 16; Length 261; Best Local Similarity 33.3%; Pred. No. 0.00018; Matches 29; Conservative 15; Mismatches 37; Indels (
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25.1%; Score 116; DB 17; Length 265;
Best Local Similarity 40.7%; Pred. No. 0.00019;
Matches 24; Conservative 10; Mismatches 25; Indels
                      ; OTHER INFORMATION: Clone ID: PAT_MRT4530_81244C.1.pep
US-10-437-963-184232
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US-10-425-114-60641
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US-10-425-115-201476
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ORGANISM: Zea mays
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US-10-425-115-201476
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LENGTH: 265
FEATURE:
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Sequence 232929, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Cao, Yongwai
APPLICANT: Cao, Yongwai
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
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  Length 294;
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US-10-425-115-232929
25.1%; Score 116; DB 15;
40.7%; Pred. No. 0.00021;
tive 10; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
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Job time : 76.8847 secs
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Query Match
Best Local Similarity
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NAME/KEY: UNSURE
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                                                                                                                                     January 26, 2005, 14:52:47; Search time 23.1356 Seconds (without alignments) 260.851 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 56, Al
Sequence 240, A
Sequence 375, A
Sequence 22463,
Sequence 8, App
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Sequence 1
Sequence 1
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(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-513-999C-7680
US-09-270-767-55035
US-09-489-039A-12408
US-09-299-63A-3
US-09-299-91A-1438
US-09-252-991A-1438
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US-09-252-991A-1438
US-09-252-991A-1438
US-09-252-991A-1438
US-09-252-991A-1738
US-09-252-991A-24083
US-09-270-767-46971
US-09-270-767-46971
US-09-270-767-46971
US-09-270-767-46971
US-09-252-991A-29113
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US-09-538-092-240
US-09-489-847-375
US-09-252-991A-22463
US-08-861-464-8
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Maximum Match 100%
Listing first 45 summaries
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463
1 MEHYRKAGSVELPAPSPMPQ....
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Gapop 10.0 , Gapext 0.5
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73.5
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Maximum DB
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No.
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Sequence 8, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3001, Appli
Sequence 2001, Appli
Sequence 2, Appli
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US-09-513-999C-7680
; Sequence 7680, Application US/09513999C
; Patent No. 678364
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Dumoniert, A.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.; Patent No. 6783661
; FILE REFERENCE: 59.US2.REG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4077, Application US/09621976

Batent No. 6639063

GENERAL INFORMATION:

APPLICANT: Johert, S.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: ESTE and Encoded Human Proteins.

TITLE OF INVENTION: ESTE and Encoded Human Proteins.

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SEQ ID NO 4077

LENGTH: 128
US-08-396-001-8
US-09-323-433A-8
US-09-323-433A-8
US-09-318-433A-8
US-09-318-4018-2
US-09-3100-2
US-09-3100-2
US-09-252-991A-28848
US-09-252-991A-28848
US-09-252-991A-28848
US-08-972-631-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Xaa = Asp, Glu, Gly, Val
US-09-621-976-4077
    TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Drosophila melanogaster
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US-09-270-767-39818
i Sequence 39818. Application US/09270767
j Patent No. 6703491
j GENERAL INFORMATION:
i TILL OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
j TILL OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
j CURRENT APPLICATION NUMBER: US/09/270,767
j CURRENT FILING DATE: 1999-03-17
j NUMBER OF SEQ ID NOS: 62517
j SOFTWARE: Patentin Ver. 2.0
j SEQ ID NO 39818
j LENGTH: 118
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                                                                                                                                                                                                                                                                                                                                                         11 ELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAVSC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DLPPEDCMPKSQKDFLWMHVKGGTKVSNVIEFAQEALNKGEHRCVVWSGSGGGVGKTISC 60
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TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 55035
                                                                                                                                                                                                                                                                                                                             1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 5.1e-42;
Matches 78; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Xaa means any amino acid US-09-270-767-39818
CURRENT APPLICATION NUMBER: US/09/513,999C
                 CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SEQ ID NO 7680
LENGTH: 78
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Patent No. 6703491
GENERAL INFORMATION:
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61 AEVLKRSHP-LYQVTRMAY 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 AEIVKRRVPGLHQLTKLRF 89
                                                                                                                                                                                                                                                                                                                                                                                                                                        61 GRAAGKAVSCAEIVKRRV 78
                                                                                                                                                                                                                                                                                                                                                                                                              GRAAGKAVSCAEIVKRRV 78
                                                                                                                                                                              ) ORGANISM: Homo sapiens
US-09-513-999C-7680
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RESULT 5
US-09-489-039A-12408
Sequence 12408, Application US/09489039A
Fatent No. 6610836
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
FRICE REPERENCE: 2000-01-27
FRICE FILING DATE: 1999-01-29
FRICE FILING DATE: 1999-01-29
FRICE FILING DATE: 1990-01-29
FRICE FILING DATE: 1990-01-29
FRICE FILING DATE: 1990-01-29
FRICE FILING DATE: 1990-01-29
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                                                                                                                                                                                                     11 ELPAPSPMPOLPPDTL----EMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAG
                                                                                                                             Ή,
                                                                                Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.3%; Score 75.5; DB 4; Length 261; 27.7%; Pred. No. 0.26; Live 18; Mismatches 31; Indels 1:
                                                                                                                             29; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: METHOD FOR THE RECOMBINANT TITLE OF INVENTION: PRODUCTION OF 1,3-PROPANEDIOL
                                                                           DB 4;
                                                                           Score 151.5; DB 4
Pred. No. 2.8e-11;
                                                                                                                          16; Mismatches
) OTHER INFORMATION: Xaa means any amino acid US-09-270-767-55035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                232 SÁMTFGTVGQSSAÞGQIAIAKLR 254
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STEPHEN K. PICATAGGIO
RAMESCH V. NAIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08968563
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ANY (KUANG-HUA) HSU
RICHARD D. LA REAU
SHARON L. HAYNIE
MARIA DIAZ-TORRES
DONALD E. TRIMBUR
GREGORY M. WHITED
VASANTHA NAGARAJAN
                                                                                                                                                                                                                                                                                               71 AEIVKRRVPGLHQLTKLRF 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Klebsiella pneumoniae
                                                                        Query Match 32.7%;
Best Local Similarity 41.8%;
Matches 33; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 16.3%
Best Local Similarity 27.74
Matches 23, Conservative
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APPLICANT:
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APPLICANT:
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2 EHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVF--SG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 271;
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Patent No. 6158716
GENERAL INFORMATION:
APPLICANT: BULTHUIS, BEN A.
GATENDY, ANTHONY A.
HAYNIE, SHARON L.
HSU, AMY K.
LAREAU, MY K.
GLYCEROL BY RECOMBINANT
                              OPERATING SYSTEM: Windows
SOFTWARE: FastENG for Windows
SOFTWARE: FastENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/969,683A
FILING DATE:
CLASSIFTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: ECT/US97/20873
FILING DATE: 13-NOV-1997
FILING DATE: 13-NOV-1997
APPLICATION NUMBER: 60/030,601
FILING DATE: 13-NOV-1996
ATTOMNEY AGENT INFORMATION:
NAME: Glaister Debra
REGISTRATION NUMBER: 33,888
RESTENCE/DOCKET NUMBER: GG 369-2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: GENENCOR INTERNATIONAL, INC.
STREET: 4 CAMBRIDGE PLACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/297,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.48;
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Pred. No. 0.
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MEDIUM TYPE: DISKETTE, 3.5 INCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1870 SOUTH WINTON ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISMS
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 28.3%;
Matches 26; Conservative 1:
            IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: ROCHESTER
STATE: NEW YORK
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 650-864-76
TELEFAX: 650-845-6504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
) ORIGINAL SOURCE:
) ORGANISM: GPP1
US-08-969-683A-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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US-09-297-928-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
15.9%; Score 73.5; DB 3; Length 271;
Best Local Similarity 28.3%; Pred. No. 0.48;
Matches 26; Conservative 13; Mismatches 32; Indels 2:
                                                                                                                                                                                                                STATE: NEW YORK
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.50 INCH DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/968,563
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 33, Application US/08969683A
Patent No. 6136576
GENERAL INFORMATION:
TITLE OF INVENTION: METHOD FOR THE RECOMBINANT
TITLE OF INVENTION: PRODUCTION OF 1,3 PROPANEDIOL
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International, Inc.
STREET: 4 Cambridge Place
STREET: 1870 South Winton road
CITY: ROADS SOUTH Winton road
STATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 AGIAAGKAAGC----KIVGIATTFDLDFLK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 SGRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQ 91
                                                                                          ZIP: 19898
ADDRESSEE: GENENCOR INTERNATIONAL, INC.
STREET: 4 CAMBRIDGE PLACE
STREET: 1870 SOUTH WINTON ROAD
CITY: ROCHESTER
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,601
FILING DATE: NOVEMBER 13, 1996
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: CR-9982
TELECOMMUNICATION INFORMATION:
TELEFHONE: 302-92-8112
TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
: 1007 MARKET STREET WILMINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 271 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A
ZIP: 14618
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: GPP1
                                                    DELAWARE
                                                                           U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-969-683A-33
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Sequence 17438 Application US/09252991A
; Sequence 17438 Application US/09252991A
; Sequence 17438 Application US/09252991A
; Patent No. 6511795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS;
; FILE REFRENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT PILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
          Parent No. 655179.

Patent No. 655179.

Patent No. 655170.

Patent No. 655170.

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 18531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 RKAGSVELPAP-----SPMPQL---PPDTLEMRVRDGSKIRNLLGLALGRLEGGSARH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 15.1%; Score 70; DB 4; Length 284; Best Local Similarity 29.0%; Pred. No. 1.4; Matches 18; Conservative 10; Mismatches 32; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 71; DB 4; Length 566;
Pred. No. 2.6;
8; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 VVFSGS-GRAAGKAVSCAEIVKRRVPG 80
Sequence 18531, Application US/09252991A
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US-09-800-729-101
Sequence 101. Application US/09800729
Patent No. 6605592
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15.3%;
28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Conservative
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Best Local Similarity
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LENGTH: 284
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Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARENGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR PLILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-02-18

PRIOR FILING DATE: 1999-07-27

NUMBER: OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 EYFITANDVKÇGKPHPEPYL------KGRNGLGFPINEQDPSKSKVVVPEDAP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 ADSPALPVQQPEQHRQPDRAGPAEGRACGAGPVRPVPG-----QPGEARHFSFLGGGTG 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 EHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVF--SG 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 AGSVELPAPSPMPQLPPD---TLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
15.9%; Score 73.5; DB 3; Length 271;
Best Local Similarity 28.3%; Pred. No. 0.48;
Matches 26; Conservative 13; Mismatches 32; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.7%; Score 72.5; DB 4; Length 290; Best Local Similarity 34.8%; Pred. No. 0.7; Matches 23; Conservative 4; Mismatches 30; Indels
                  CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/03602
FILING DATE: NOVEMBER: 13, 1996
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: 37,692
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-892-8112
TELEFONS: 50773-0164
TELERA: 302-773-0164
TELERA: 50773-0164
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                203 AGIAAGKAAGC-----KIVGIATTFDLDFLK 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 SGRAAGKAVSCAEIVKRRVPGLHQLTKLRFLQ 91
                                                                                                                                                                                                                                                                                                                                                               | LENGTH: 271 amino acids | TPEE: amino acids | TPEE: amino acid | STRANDEDNESS: unknown | TOPOLOGY: unknown | MOLECULE TYPE: protein | SEQUENCE DESCRIPTION: SEQ ID NO: 14: US-09-297-928-14
FILING DATE: 11-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
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US-09-252-991A-18531
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LENGTH: 290
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Gaps

36;

Gaps

Gaps

16;

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5 RKAGSVELPAPSPMPQLPPDTLEM------RVRDGSKIRNLLGLALGRLEGGSA 52
                                                                                                                                                                                                                                                                                                                                                                       Query Match 14.9%; Score 69; DB 3; Length 639; Best Local Similarity 25.6%; Pred. No. 5.4; Matches 22; Conservative 15; Mismatches 33; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.9%; Score 69; DB 4
25.6%; Pred. No. 5.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Allen, Steve
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/854,731
CURRENT APPLICATION NUMBER: 60/092,438
FRIOR APPLICATION NUMBER: 60/092,438
FRIOR FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 17
                                APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: January 26, 2005, 15:08:52
Job time : 24.1356 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 HLCV----ERATGKELACKSILKRKL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              168 HLCV----ERATGKELACKSILKRKL 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 RHVVFSGSGRAAGKAVSCAEIVKRRV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53 RHVVFSGSGRAAGKAVSCAEIVKRRV 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 17, Application US/09854731; Patent No. 6794561; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22; Conservative
              APPLICANT: Allen, Steve
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                                                                                                                                                                                                                                                                            TYPE: PRT

ORGANISM: Zea mays
US-09-347-801-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                                                                                                                       SEQ ID NO 17
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Patent No. 6380370

GENERAL INFORMATION:
FALL SPECIAL SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTC-007

CURRENT PELING DATE: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-11-08

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

LENGTH: 482
                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (86)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (146)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 14.9%; Score 69; DB 4; Length 183; Best Local Similarity 32.8%; Pred. No. 1.1; Matches 20; Conservative 5; Mismatches 16; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 14.9%; Score 69; DB 3; Length 482; Il Similarity 32.7%; Pred. No. 3.8; 17; Conservative 9; Mismatches 22; Indels
APPLICANT: Ni et al.
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION WIMBER: US/09/800,729
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION WIMBER: PCT/US00/26013
PRIOR FILING DATE: 2000-09-22
PRIOR PILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Staphylococcus epidermidis US-09-134-001C-4309
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US-09-347-801-17
Sequence 17, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: SITE
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                                                                                                                                                                                                                                                       SEQ ID NO 101
LENGTH: 183
                                                                                                                                                                                                                                                                                                      TYPE: PRT
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5 RKAGSVELPAPSPMPQLPPDTLEM-----RVRDGSKIRNLLGLALGRLEGGSA 52
                            Gaps
                            16;
DB 4; Length 639;
                           33; Indels
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January 26, 2005, 15:09:58; Search time 39 Seconds (without alignments) 224.506 Million cell updates/sec
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463
1 MEHYRKAGSVELPAPSPMPQ.....EIVKRRVPGLHQLTKLRFLQ 91
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                       283416 segs, 96216763 residues
                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 91
                                                                                                                                                                                             Title:
Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Database :

Description	toditorial Constitution	anion exchanger 3	conserved hypothet				ы	hypothetical prote		•	hypothetical prote	_	_	_	_	_	_	_	_	'	hypothetical prote	early ElB 9K prote		gp42 protein - Myc			cell division topo	conserved hypothet	probable protoporp
SUMMARIES		138497	C69383	173095	C84802	G75509	T28356	G84527	E75144	183200	H82855	E64326	AE2239	AF2125	S48815	D96493	AB1897	G95891	E65027	183199	S08493	WMAD9	AB0804	H72804	B40513	E30010	D82136	AB3204	T34721
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% Query Match	14 1		12.1	11.8		11.1	ä	ö	ö	10.6	ö	٥.	10.5	10.4	。	ö	ö	10.2	。	ö	ö	10.2			٠	9.9	•	9.9	
Score	65.5	·	26	54.5	51.5	-	S	50.5	20	49	4	49	48.5	48	4	47.5	47	47	47	47	47	47	47	46	46	46	46	46	45.5
Result No.	-	10	'n	4	2	9	7	σ0	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

conserved hypothet	flhB-related prote	major histocompati	hypothetical prote	hypothetical prote	hypothetical prote	photosystem I iron	hypothetical 7.7K	hypothetical prote	probable small sec	hypothetical prote	basic fibroblast g	hypothetical prote	ribosomal protein	zinc finger protei	hypothetical prote
C82684	D71268	I54529	T12907	AC3575	AG3196	834540	D31844	T16647	T36927	AI3287	B48834	T06016	A64386	137964	AE2949
7	Н	0	~	N	7	~	~	~	7	~	~	~	0	7	7
75	83	57	72	75	79	80	99	84	88	88	54	59	52	26	69
œ	8	7.4	7.6	9.7	7.6	7.6	9.6	9.6	9.6	9.6	9 .S	و. د	9.4	9.4	4.6
e,	σ	-													
45.5 9.	45.5	45	45	45	45	45	44.5	44.5	44.5	44.5	44	44	43.5	43.5	43.5

ALIGNMENTS

RESULT 1

	C69494
	conserved hypothetical protein AF1956 - Archaeoglobus fulgidus
	Cyptecies: Archaeoglobus lightup Cybite: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
	C.K.Clenk, H.D.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodso.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F
-	Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
	A; Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Moese, C.R.: Venter, J.C.
	A, Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae. A, Reference number: A69250; MUID: 98049343; PMID: 9389475
	A.Accession: C69494 A.Status: preliminary; nucleic acid sequence not shown; translation not shown
	A;Molecule type: DNA A;Residues: 1-89 «KLE» A;Cross-references: UNIPROT:O28323; GB:AE000968; GB:AE000782; NID:q2689291; PIDN:AAB892
	C; Superfamily: Archaeal histone-like protein, Alba type
	Query Match Best Local Similarity 41.2%; Pred. No. 6.3; Matches 21; Conservative 8; Mismatches 19; Indels 3; Gaps 3;
	OY 33 GSK-IRNLLGLALGRLEGGSARHVVFSGSGRAAGKAVSGAEIVKRR-VPGL 81
	Db 9 GNKPVMNYVLATLTQLNEG-ADEVVIKARGRAISRAVDVAEIVRNRFMPGV 58
	RESULT 2
	and exchanger 3 cardiac isoform - human (fragment)
	C.Accession: 13447
	Rygannoukakos, D.; Stuart-Tilley, A.; Fernandez, H.; Fey, P.; Duyk, G.; Alper, S.
	A.Title: Molecular cloning, expression, and chromosomal localization of two isoforms of A.Reference number: 138496; MUID:95008042; PMID:7923606
	A,Accession: 138497 A,Status: preliminary; translated from GB/EMBL/DDBJ
	A;Cross-references: UNIPROT:Q12835; EMBL:U05597; NID:g476223; PIDN:AAA50749.1; PID:g476 C;Superfamily: band 3 anion transport protein C;Reywords: cardiac muscle; heart
	Query Match 13.0%; Score 60; DB 2; Length 72;
	best Local Similarity 43.6%; Pred. No. 19; Matches 17; Conservative 1; Mismatches 15; Indels 6; Gaps 1;

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hypothetical protein At2g38210 [imported] - Arabidopsis thaliana
CiSpecias: Arabidopsis thaliana (mouse-ear cress)
CiSpecias: Arabidopsis thaliana (mouse-ear cress)
CiDate: 02-Peb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
CiAccession: C84802
M: KiLin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M: Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.A.; Reference number: A4420; MulD:20083487; PMID:10617197
A;Accession: C84802
A;Accession: C84802
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-79 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:080446; GB:AE002093; NID:g3335369; PIDN:AAC27170.1; GSPDB:GN
C;Genetics:
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A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Species: Deinococcus radiodurans
C;Spacession: G75509
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R. M.; Shan, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORP MSV195 ALI motif gene family protein - Melanoplus sanguinipes entomopoxvirus C; Species: Melanoplus sanguinipes entomopoxvirus C; Species: J-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004 C; Accession: T28356 Well and E.R.; Lu, Z.; Oma, E.; Kutish, G.P.; Rock, D.L. R; Afonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.P.; Rock, D.L. A; Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A; Reference number: Z20484; MUID:99102612; PMID:9847359
A; Accession: T28356
A; Accession: T28356
A; Accession: T28556
A; Accessi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40 LGLALGRLEGGSARHVVFSGSGRAAGKAVSCAEIVKRRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 51.5; DB 2;
Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 51.5; DB 2;
Pred. No. 1.9e+02;
4; Mismatches 14;
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Best Local Similarity 40.0%;
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 11.1%;
1 Similarity 35.4%;
17; Conservative
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Matches 17; Conserva
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A;Molecule type: DNA
A;Residues: 1-90 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: G75509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: At2g38210
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 1
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C;Species: Loris tardigradus (slender loris)
C;Species: Loris tardigradus (slender loris)
C;Species: Loris tardigradus (slender loris)
C;Species: O'Dul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I73095; 173095
R;Figueroa, F; O'Nuigin, C; Tichy, H.; Klein, J.
J. Immunol. 152, 4455-4465, 1994
A;Title: The origin of the primate Mnc-DRB genes and allelic lineages as deduced from the A;Reference number: I5627; MUID:94209665; PMID:8157963
A;Accession: I73095
A;Residues: 1-83 - RES>
A;Cross-references: UNIPROT:Q30547; UNIPROT:Q30543; EMBL:Z27126; NID:g415838; PIDN:CAARIA;NOCES - BENEWOODS
A;Noce: DRB-W2005
A;Molecule type: DNA
A;Residues: 1-83 - RES>
A;Cross-references: EMBL:Z27161; NID:g415844; PID:g415845
A;Note: DRB-W2006
                                                                                                                                                                                                                                                                                                                                                                              C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
C;Caccesion: C69383
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson is Fleischmann, R.D.; Quackenbush, J.F.; White, O.; Nelson, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Avture 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S. A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaed archaecter number: A69250; MUID:98049343; PMID:9389475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-89 «KLE»
A;Cross-references: UNIPROT:O29195; GB:AE001029; GB:AE000782; NID:g2689352; PIDN:AAB9017
C;Superfamily: Archaeal histone-like protein, Alba type
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A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                  Species: Archaeoglobus fulgidus
Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 16-Aug-2004
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7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein AF1067 - Archaeoglobus fulgidus
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11.8%; Score 54.5; DB 2; Length
Best Local Similarity 26.0%; Pred. No. 84;
Matches 20; Conservative 12; Mismatches 34; Indels
                  45
                                                               PAPSPMPQLPPDTLEMRVRD---
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C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C;Accession: E64326
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
                  syntaxin 3E - mouse
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
C;Accession: 183200
R;Ibaraki, K.; Horikawa, H.P.; Morita, T.; Mori, H.; Sakimura, K.; Mishina, M.; Saisu, Biochem. Biophys. Res. Commun. 211, 997-1005, 1995
A;Title: Identification of four different forms of syntaxin 3.
A;Reference number: 160170; MUID:95321968; PMID:7598732
A;Accession: 183200
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Reteure preliminary; translated from A;Residues: 1-86 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein XF0041 [imported] - Xylella fastidiosa (strain 9a5c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:D38375; NID:g924275; PIDN:BAA07454.1; PID:g924276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 10.6%; Score 49; DB 2; Length 86; 1 Similarity 42.3%; Pred. No. 3.38+02; 11; Conservative 5; Mismatches 10; Indela
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : | : | | : | | | | : | : | 3 VEEAKKLYSIILSAPIPEPKLPRNPL 78
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Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Filth, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Kao, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tallon, L. Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-85 <STO>
A;Cross-references: UNIPROT:Q9SUP7; GB:AE002093; NID:g4544379; PIDN:AAD22290.1; GSPDB:GN
C;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 2
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9V1W2; GB:AJ248284; GB:AL096836; NID:g5457730; PIDN:CAB4923
A;Experimental source: strain Orsay
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein At2g15340 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: G84527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 AGSVELPAPSPMPQ-----LPPDTLEMRVRDGSKIRNLLGLA-LGRLEGG
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Pred. No. 2.3e+02;
6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30 VRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAVSCAEIVKRRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein PAB3086 - Pyrococcus abyssi (strain Orsay)
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                                                                                                                                                                    Length 87;
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                                                                                                                                                                    Score 51; DB 2; Length 87;
Pred. No. 2.1e+02;
5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                   54 HVVFSGSGRAAGKAVSCAEIVKRRVP 79
                                                                                                                                                                                                                                                                                                                                                        |:| :: ||:|||:| | 14 HIVIDNNNKVLFKAKNCAEILKYTNP 39
                                                                                                                                                                 Query Match
Best Local Similarity 38.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 36.4%;
Matches 20; Conservative
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                                                           C;Genetics:
A;Note: MSV195
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14;

Length 80; 14; Indels

Score 48; DB 2; I Pred. No. 3.9e+02; 5; Mismatches 14;

10.4%;

20

6 KAGSVELP----APSPMPQL-PPDTLEMRVRDGSKIRNLLGLALGRLEGG

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Search completed: January 26, 2005, 15:35:25 Job time: 40 secs
                                                                                        Query Match
Best Local Similarity 34.0°
Matches 17; Conservative
                                   A;Gene: as12557
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; Reich, C.I.; Overbeek, R.; Kirkness, B.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.; Fron, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A. Science. 273, 1058-1073, 1996
A.; Authors: Kaine, B. Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.A.; Authors: Kaine, Borome sequence of the methanogenic archaeon, Methanococcus jannaschii A; Reference number: A64300; MUD: 96337999; PMID: 8688087
A; Reference number: B64326
A; Status: preliminary; nucleic acid sequence not shown; translation not shown A; Mesidues: 1-87 kBUL>
A; Cossi-references: UNIPROT: 057665; GB: U67477; GB: L77117; NID: G1590349; PIDN: AAB98197.1; C; Genetics:
A; Map position: FORZ03759-204022
C; Superfamily: Archaeal histone-like protein, Alba type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein agr3468 [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
C;Species: Nostoc sp. pCC 7120
C;Species: Nostoc sp. pCC 7120
C;Bate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE239
C;Accession: AE239
C;Accession: AE239
C;Accession: AE239
C;Accession: AE239
C;Accession: AE239
DNA Res. 8, 205-213, 2001
DNA Res. 8, 205-213, 2001
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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C.Species: Nostoc sp. PCC 7120
C.Species: Nostoc sp. Errain PCC 7120
C.Species: Nostoc sp. strain PCC 7120
C.Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C.Accession: AF2125
K.Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
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10.5%; Score 48.5; DB 2; Length 83;
Best Local Similarity 28.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 5; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.6%; Score 49; DB 2; Length 87; ilarity 39.1%; Pred. No. 3.4e+02; Conservative 5; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55 VVFSGSGRAAGKAVSCAEIVKRR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 VIIKARGKAINKAVDVAEMIRNR 51
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Best Local Similarity
Matches 9, Conserv
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-80 <KUR>
A;Cross-references: UNIPROT:Q8YU04; GB:BA000019; PIDN:BAB74256.1; PID:g17131649; GSPDB:CC;Genetics:

A; Accession: AF2125

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Apportetical protein 3 - turkey herpesvirus
C.Species: turkey is a sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C.Species: A.Smith, G.G.; Zelnik, V.V.; Ross, N.N.
R.Smith, G.G.; Zelnik, V.V.; Ross, N.N.
A.Speciece: the EMBL Data Library, October 1994
A.Description: Gene organization in herpes virus of turkey: identification of a novel OR
A.Reference number: 488113
A.Accession: S48811
A.Status: preliminary
A.Status: preliminary
A.Status: DAA
A.Residues: 1-84 <SMI>
A.Residues: 1-84 <SMI>
A.Residues: 1-84 <SMI>
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10 KVRVVALPPYIKTADPMPRRPPDVIQL----GEE----GIVLDRRPGG 50
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10.4%; Score 48; DB 2; Length 84;
Best Local Similarity 38.5%; Pred. No. 4.1e+02;
Matches 15; Conservative 5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 GSKIRNLLGLALGRLEGG--SARHVVFSGSGRAAGKAVS 69
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January 26, 2005, 15:08:58 ; Search time 193 Seconds (without alignments) 271.291 Million cell updates/sec
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463
1 MEHYRKAGSVELPAPSPMPQ......EIVKRRVPGLHQLTKLRFLQ 91
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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239185 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 91

1825181 segs, 575374646 residues

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

SUMMARIES

ription	323 archaeoglob		tadpo		0x0 bufo marinu	<pre>%x2 leptodactyl</pre>				z6 bufo marinu	28 rana tempor		arabi		.95 archaeoglob		'n	.0112 oryza sat		396 oryza sativ	ory	03	٦	47 loris tardi	nt9 homo sapien	Aah69658 homo sapi	Aah69757 homo sapi	5	bufo bu		z2 bufo bufo u
Desc	02832	012835	Q9 j 9w4	2.60 3.60	09 <u>.</u>	09 j 9x2	Q9j8	260 260	9 j 60	5 E 60	2 60 2 60	99.je	1860 1860	Q92mc1	029195	Q883x2	06z5d	Bad101	027527	062836	Bad	Bad(Q30543	Q30547	Q9uht 9	Aahe	Aah(Aahe	9 j 6 O	99je	Q9j9z2
SUMMARIES	ALB2 ARCFU	Q128 <u>3</u> 5	Q9J9W4	Q9J9W8	03676Q	Q9J9X2	9X6£6Q	Q9J9Y2	Q9J9Y4	926260	Q9J9Z8	Q9JA00	Q9SFC3	Q92MC1	ALB1_ARCFU	Q8S3 <u>X</u> 2	Q625DS	BAD10112	ALBA METTH	062896	BAD07703	BAD07903	Q30543	030547	PH68_HUMAN	AAH69658	AAH69757	AAH69775	Q9J9Y8	Q9J9Z0	Q9J9Z2
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% Query Match Length	1	13.0		•	•	•	•	•		12.5	12.5	12.5	12.4	12.1		•	•		12.0	11.9	11.9	٠	٠		11.7	11.7	11.7	11.7	11.6	11.6	11.6
Score		9	58	58	58	28	28	28	28	28	28		57.5	99		S	55.5	S	55.5	52	22		54.5	4.	54		54	54	53.5	'n	53.5
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Q6z8s3 oryza sativ Bad10039 orvza sat	Q99pm8 mus musculu Q96tz4 neurospora		_	Osu446 arabidopsis Q9rwz8 deinococcus	- 0	09j9y0 doctor fish	Q9j9y6 catfish iri	Q9j9z4 bohle irido
Q6Z8S3 BAD10039	Q99PM8 Q96TZ4	Q61JF3 Q6FVB9	0861193	Q9RWZ8	Q9J9W6 Q9J9X4	Q909Y0	Q9J9Y6	Q9J9Z4
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11.6	11.4	11.3	11:2	11.1	11.0	11.0	11.0	11.0
53.5	ម ម ម	52.5	22	51.5	512	21	21	51
32	34 35	36	8 6	J 4.	4 4 2 7	43	44	45

ALIGNMENTS

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MEDLINE=20214220; PubMed=10752555;
Hyatt A.D., Gould A.R., Zupanovic Z., Cunningham A.A.,
Hengetberger S., Whittington R.J., Kattenbelt J., Coupar B.E.H.;
"Comparative studies of piscine and amphibian iridoviruses.";
Arch. Virol. 145:301-331(2000).
EMBL, AF157680; AAF64591.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=20214220; PubMed=10752555;

Hyatt A.D., Gould A.R., Zupanovic Z., Cunningham A.A.,

Hengstberger S., Whittington R.J., Kattenbelt J., Coupar B.E.H.;

"Comparative studies of piscine and amphibian iridoviruses.";

Arch. Virol. 145:301-331 (2000).

EMBL, AF157676; AAP64587.1;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
Hypothetical protein (Fragment).
Buffo marinus Venezuelan iridovirus 2.
Viruses; deDNA viruses, no RNA stage; Iridoviridae; Iridovirus;
Bufo iridoviruses.
                                                                                    01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment)
Tadpole edema virus
Viruses, daDNA viruses, no RNA stage; Iridoviridae; Ranavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 71;
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Pred. No. 2.6e+02;
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Pred. No. 2.6e+02;
6; Mismatches 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Conservative
                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
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NON TER 1
NON_TER 71 7
                                                                                                                                                                                                                                             NCBI_TaxID=100214;
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Best Local Similarity
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nes 15; Conserv
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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01-OCT-2000 (
01-OCT-2003 (
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NON TER
SEQUENCE
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Matches
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Q9J9X0
                  09J9W4
                                               DDT TO DD
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K->R,O,M: Less stable tetramers;
decreased ability to bind DNA.
L->R: Less stable tetramers; decreased
ability to bind DNA.
F->R: Less stable tetramers; decreased
ability to bind DNA.
96071A4C48CB8ED7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUB-Heart;
MEDLINE-95008042; PubMed=7923606;
Yannoukakos D., Stuart-Tilley A., Fernandez H., Fey P., Duyk G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning, expression, and chromosomal localization of isoforms of the AE3 anion exchanger from human heart."; Circ. Res. 75:603-614(1994).
EMBL; U05597; AAA50749.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 GSK-IRNLLGLALGRLEGGSARHVVFSGSGRAAGKAVSCAEIVKRR-VPGL 81
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N->A: Slight decrease in ability
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 89;
                                                                                                                                                                                                                                                                                                                         Probom; PD010497; DUF78; 1.
TIGRPAMS; TIGR00285; DUF78; 1.
TOB DETLUCTURE; Acetylation; Complete proteome; DNA-binding; RNA-binding. 11 N6-acetylveine (Rv similaxit.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65.5; DB 1; Length B
Pred. No. 55;
8; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60; DB 2; Length 72;
Pred. No. 1.6e+02;
1; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 AA; 7667 MW; 95DCC64DB1B30718 CRC64;
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Last sequence update)
Last annotation update)
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|PAPSPRDSLAPEDLEMFVLDFEDGDLWESIRGQLGPMAG
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence upd,
01-UJW-2003 (TrEMBLrel. 24, Last annotation up
Anion exchanger 3 cardiac isoform (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 AA.
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                                                                                                                                 EMBL; AE000968; AAB89299.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.1%;
ilarity 41.2%;
Conservative
                                                                                                                                                                                                                                  TIGR; AF1956; -.
HAMAP; MF_01122; -; 1.
InterPro; IPR002775; DUF78.
Pfam; PF01918; DUF78; 1.
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9894 MW;
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1NFJ; X-ray; A=1-89.
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Best Local Similarity
Matches 17; Conserv
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RESULT 2

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                    Hyatt A.D., Gould A.R., Zupanovic Z., Cunningham A.A., Hengstberger S., Whittington R.J., Kattenbelt J., Coupar B.E.H.; Comparative studies of piscine and amphibian iridoviruses.", Arch. Virol. 145:301-31(2000).

EMBL; AF157668; AAF64579.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

BEDINES-2014220; PubMed=10752555;

Hyatt A.D., Gould A.R., Zupanovic Z., Cunningham A.A.,

Hengstberger S., Whittington R.J., Kattenbelt J., Coupar B.E.H.;

Hengstberive studies of piscine and amphibian iridoviruses.";

Arch. Virol. 145:301-31(2000).

EMBL, AF157662; AAF64573.1;
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MEDLINE=20214220; PubMed=10752555;
Hyatt A.D., Gould A.R., Zupanovic Z., Cunningham A.A.,
Hengstberger S., Whittington R.J., Kattenbelt J., Coupar B.E.H.;
Hengstberive studies of piscine and amphibian iridoviruses.";
Arch. Virol. 145:301-331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical protein (Fragment).
Bufo marinus Venezuelan iridovirus 4.
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus;
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Hypothetical protein (Fragment)

Bufo marinus Venezuelan iridovirus 6.

Viruses; dabDNA viruses, no RNA stage; Iridoviridae; Iridovirus;

Bufo iridoviruses.

NCBI_TAXID=105556;
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                                                                                                                                                                                                          Length 71;
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                                                                                                                                                                     71 AA; 7845 MW; 88A4EBF82A2EDDC0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                     26 HHPVSGTQECKLVVAQSPGPQLPPSPKLRFRTRDNQEV
                                                                                                                                                                                                       Score 58; DB 2; I
Pred. No. 2.6e+02;
6; Mismatches 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58;
Pred. No.
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       MEDLINE=20214220; PubMed=10752555;
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39.5%;
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                                                                                                                                                                                                                                              15; Conservative
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NON TER 1
NON TER 71
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NCBI_TaxID=105555;
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                                                                                                      MEDLINE=20214220; PubMed=10752555; MEDLINE=20214220; PubMed=10752555; Mytting A.B., Gould A.R., Zupanovic Z., Cunningham A.A., Hyatt A.D., Gould A.R., Whittington R.J., Kattenbelt J., Coupar B.E.H.; Hengstberger S., Whittington R.J., Kattenbelt J., Coupar B.E.H.; "Comparative studies of piscine and amphibian iridoviruses."; Arch. Virol. 145:301-331(2000).

EMBL, AF157674; AAF64585.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

BEDINRE-20214220; PubMed=10752555;

Hyatt A.D., Gould A.R., Zupanovic Z., Cunningham A.A.,

Hengstberger S., Whittington R.J., Kattenbelt J., Coupar B.E.H.;

Hengstberger S., Whittington R.J., Kattenbelt J., Coupar B.E.H.;

Comparative studies of piscine and amphibian iridoviruses.";

Arch. Virol. 145:301-331(2000).

EMBL; AF157672; AAF64583.1;
Hypothetical protein (Fragment).
Bufo marinus Venezuelan iridovirus 3.
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Leptodactylus Venezuelan iridovirus 1.
Viruses, dspNA viruses, no RNA stage; Iridoviridae; Ranavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein (Fragment).
Frog virus 3 (FV3).
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Ranavirus.
                                                                                                                                                                                                                                                                                                                                  Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 71;
                                                                                                                                                                                                                                                                                                                                  Score 58; DB 2; Length 71;
Pred. No. 2.6e+02;
6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13; Indels
                                                                                                                                                                                                                                                                                              71 AA; 7845 MW; 88A4EBF82A2EDDC0 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                               3 HYRKAGSVE---LPAPSPMPQLPPD-TLEMRVRDGSKI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 HYRKAGSVE---LPAPSPMPQLPPD-TLEMRVRDGSKI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 58; DB 2; I
Pred. No. 2.6e+02;
6; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 AA.
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llarity 39.5%;
Conservative (
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 39.5%;
Matches 15; Conservative
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nes 15, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=100219;
                                                                         NCBI_TaxID=105554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10493;
                                                       Bufo iridoviruses
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SEQUENCE
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Q9J9X6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Query Match
Best Local Similarity 39.5
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                          Hypothetical protein.
NON TER 1
NON_TER 71 7
                                                                                                                                                                                                                       Viruses; dsDNA viru
NCBL_TaxID=105557;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3702;
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                                                                                                                                                 Q9JA00;
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                                                                                                              RESULT 12
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MEDLINE=20214220; PubMed=10752555;
Hyatt A.D., Gould A.R., Zupanovic Z., Cunningham A.A.,
Hengstberger S., Whitington R.J., Kattenbelt J., Coupar B.E.H.;
"Comparative studies of piscine and amphibian iridoviruses.";
Arch. Virol. 145:301-331(2000).
BMBL; AFI57646; AAF64557.1; -.
                                                                                                                                                                                                                                                                                                                                                                           Coupar B.E.H.;
                                                                                                                                                                                                                                                            Hypothetical protein (Fragment).
Bufo marinus Venezuelan iridovirus 1.
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus;
                                                                                                  4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment)
Rana temporaria United Kingdom iridovirus 2.
Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Iridovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4,
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=20214220; PubMed=10752555;
Hyatt A.D., Gould A.R., Zupanovic Z., Cunningham A.A.,
Hengstberger S., Whittington R.J., Kattenbelt J., Coupar B.E.H.
"Comparative studies of piscine and amphibian iridoviruses.";
Arch. Virol. 145:301-331(2000).
EMBL; AF157648; AAF64559.1; -.
                                                                         Length 71;
                                                                                  2.6e+02;
ches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 58; DB 2; Length 71;
Pred. No. 2.6e+02;
6; Mismatches 13; Indels
                                               88A4EBF82A2EDDC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 AA; 7845 MW; 88A4EBF82A2EDDC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7845 MW; 88A4EBF82A2EDDC0 CRC64;
                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                    3 HYRKAGSVE---LPAPSPMPQLPPD-TLEMRVRDGSKI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 HYRKAGSVE---LPAPSPMPOLPPD-TLEMRVRDGSKI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
                                                                                              6; Mismatches
                                                                                                                                                                                                        71 AA.
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                                                                       Score 58;
Pred. No. 2
                                                                       12.5%;
39.5%;
                                            7845 MW;
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1 Similarity 39.5%;
15; Conservative
EMBL; AF157660; AAF64571.1;
                                                                  Query Match 12.5
Best Local Similarity 39.5
Matches 15; Conservative
                                                                                                                                                                                                       PRELIMINARY;
            Hypothetical protein.
NON_TER 1
NON_TER 71
SEQUENCE 71 AA; 78
                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
                                                                                                                                                                                                                                                                                                             NCBI_TaxID=105552;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=105558;
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                                                                                                                                                                                                                                                                                                  Bufo iridoviruses
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NON TER
SEQUENCE
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09J9Z6;
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Matches
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                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE=20214220; PubMed=10752555;

Hyatt A.D., Gould A.R., Zupanovic Z., Cunningham A.A.,
Hengstberger S., Whittington R.J., Kattenbelt J., Coupar B.E.H.;
"Comparative studies of piscine and amphibian iridoviruses.";
Arch. Virol. 145:301-331(2000).

EMBL; AFIS7644; AAF64555.1; -.
                                                                                                                                                                                                                                                             OCCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypochetical protein (Fragment)
Rana temporaria United Kingdom iridovirus 1.
Viruses; dsDNA viruses, no RNA stage; Iridovirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Lin X., Kaul S., Town C.D., Benito M.-I., Creasy T.H., Haas
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
    Length 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 71;
                                        13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ecker J.R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 AA; 7845 MW; 88A4EBF82A2EDDC0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
                                                                               3 HYRKAGSVE---LPAPSPMPQLPPD-TLEMRVRDGSKI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 HYRKAGSVE---LPAPSPMPQLPPD-TLEMRVRDGSKI 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                           26 HHPVSGTQECKLVVAQSPGPQLPPSPKLRFRTRDNQEV
12.5%; Score 58; DB 2; 139.5%; Pred. No. 2.6e+02; ive 6; Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 HHPVSGTQECKLVVAQSPGPQLPPSPKLRFRTRDNQEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 58; DB 2;
Pred. No. 2.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 39.5
Matches 15, Conservative
                                                                                                                                                                                                                               PRELIMINARY;
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NCBI_TaxID=2234;
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ALB1_ARCFU
ID _ALB1_ARCFU
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            SKARARARA
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
Ishida J., Jang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Barusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                    Haas B.J., Volfovsky N., Town C.D., Troukhan M., Alexandrov N., Feldmann K.A., Flavell R.B., White O., Salzberg S.L., "Full-length messenger RNA sequences greatly improve genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41 GLALGRIEGGSARHVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKLRFL 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brover V., Troukhan M., Alexandrov N., Lu Y.-P., Flavell R., Feldmann K.,
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 10, Last annotation update)
HYPOTHETICAL TRANSMEMBRANE PROTEIN.
OrderedLocusNames-R02706; ORFNames-SMC00666;
Rhizobium mellioti (Sinorhizobium mellioti).
Rhizobiaceae, Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 74;
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7368 MW; 44410B581F4D51ED CRC64;
                                                                                                                                                                                                    Genome Biol. 3:RESEARCH0029-RESEARCH0029(2002)
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Pred. No. 3e+02;
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MEDLINE=21368234; PubMed=11474104;
                                                         MEDLINE=22088475; PubMed=12093376;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AC013483; AAF21201.1; -. EMBL; AY060549; AAL31180.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.4%;
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Matches 16; Conservative
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13 GVAVGGALGG-
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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RY SEQUENCE FROM N.A.

STRAIN=VC-16 / DSM 4304 / ATCC 49558;

RX ALLINE=9049343; PubMed=9389475; DOI=10.1038/37052;

RX ALLINE=9049343; PubMed=9389475; DOI=10.1038/37052;

RA Ketchum K.A., Dodgon R.A., Tomb J.-F., White O., Nelson K.E.,

RA Ketchum K.A., Dodgon R.A., Gwinn M.L., Hickey E.K., Peterson J.D.,

RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,

RA Richardson D.L., Releventy B.A., McKenney K., Adams M.D., Loftus B.J.,

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.J.,

RA Kirkness E.F., Dougherty B.A., Wekenney K., Adams M.D., Loftus B.J.,

RA Corton L., Overbeek R., Gocarne J.D., Weidman J.F., McDonald L.A.,

RA Sykes S.M., Sadow P.W., D., Spriggs T., Artiach P., Kaine B.P.,

RA Sykes S.M., Sadow P.W., Olsen G.J., Fraser C.M., Smith H.O.,

RA Woese C.R., Venter J.C.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outeration the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SUBCELLULAR LOCATION: Cytoplasmic (Probable).
FTM: Acetylated. Deacetylation by the SIR2-homolog deacetylase may regulate its activity (By similarity).
SIMILARITY: Belongs to the archaeal histone-like Alba family.
Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godfeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puchler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F., Sinorhizobium meliloti strain 1021.", Weidner S., Galibert F., Sinorhizobium meliloti strain 1021.", Berson S., Galibert F., EMBL, ALS91791, CAC47285.1; -. GO, GO:0016021, Cintegral to membrane; IEA. GO, GO:0016021, Cintegral to membrane; IEA. Sequence 77 As, 8618 MW; 2CEA7D9103FIEAEB CRC64;
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Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 PSPMPQLPPDTLEMR----VRDGSKIRNLLGLALGRLEGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 56; DB 2; I
Pred. No. 4.5e+02;
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10-OCT-2003 (Rel. 42, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
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Matches 18; Conservative
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Search completed: January 26, 2005, 15:34:39 Job time : 194 secs

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January 26, 2005, 15:07:38; Search time 156 Seconds (without alignments) 209.259 Million cell updates/sec
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463
1 MEHYRKAGSVELPAPSPMPQ......EIVKRRVPGLHQLTKLRFLQ
5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                                   2002273 seqs, 358729299 residues
version :
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Maximum Match 100%
Listing first 45 summaries
                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
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length: 91
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DB seq
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. score and is

SUMMARIES

Description	Aay11950 Human S'	Aaq03599 Human sec	Aag36978 Arabidops	-	Adl71771 Novel hum	Adn99364 Novel hum	Adg22762 Cyanophag	6			Abg00727 Novel hum	Human		Abb43040 Peptide #	Aam36870 Peptide #		Aam63945 Human bra	Abq58446 Human liv	Abg18684 Novel hum		Ado20465 Human PRO	Aam84673 Human imm	Aau57537 Propionib	Abm54056 Propionib	Aag53244 Arabidops
ID		AAG03599	AAG36978	AAY91690	ADL71771	ADN99364	ADG22762	AAG34486	AAG58753	AAG15942	ABG00727	ABP10404	AAG64347	ABB43040	AAM36870	AAM76763	AAM63945	ABG58446	ABG18684	AAM86389	AD020465	AAM84673	AAU57537	ABM54056	AAG53244
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Score	402	395	119	67	67	62.5	62	61.5	57.5	57.5	57.5	52	54	53.5	53.5	53.5	53.5	53.5	53.5	23	53		52.5	52.5	52.5
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	27	52.5		11.3	77	4	AAU64906	Aau64906	Propionib	
	28	N		1.3	77	ø	ABM61425	Abm61425	Propionib	
	29	25		1.2	71	œ	ABO58355	Abo58355		
	30	52		7.7	80	4	AAU53651	Aau53651		
	31	52		1.2	80	ø	ABMS0170	Abm50170		
	32	52		1.2	81	4	AAM95345	Aam95345		
	33	52		1.2	81	4	ABB96039	Abb96039	Human tes	
	34	25		1.2	87	4	AAM92262	Aam92262	Human dig	
	35	51.5		۲.1	61	4	AAU53022	Aau53022		
	36	51.5		1.1	61	9	ABM49541	Abm49541	Propionib	
	37	51.5		1.1	65	m	AAG31725	Aag31725		
	38	51.5		1.1	79	٣	AAG31723	Aag31723	Arabidops	
	39	21		0.1	72	9	ABP80069	Abp80069	N. gonorr	
	40	51		0.1	75	4	AAM13691	Aam13691	Peptide #	
	41	51		0.1	75	4	ABB32622	Abb32622	a	
	42	51		0.1	75	4	AAM26091	Aam26091	#	
	43	21		0.1	75	4	ABB27471	Abb27471	Human pep	
	44	21		0.1	75	4	ABB18120	Abb18120	Protein #	
	45	21		0.1	75	4	AAM65829	Aam65829	Human bon	
							ALIGNMENTS			
RESU AAY1	RESULT 1	į				_				
e X	AAXTT	950	всапс	Jara;	AAY11950 standard; protein; 79	; :	79 AA.			
Ą	AAY11950;	950;								

Human; secreted protein, EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; prostate; upstream regulatory sequence; cyrokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemotactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition. New isolated prostate-derived nucleic acids - used to develop products which may have cytokine, immune regulatory, haematopoiesis regulating, anti-inflammatory or tumour inhibition activity. Lacroix B; Human 5' EST secreted protein SEQ ID No: 550. Duclert A, 98WO-IB001232 97US-00905144 (first entry) Dumas Milne Edwards J, WPI; 1999-153780/13. N-PSDB; AAX40672. (GEST) GENSET. 01-AUG-1997; Homo sapiens WO9906550-A2. 31-JUL-1998; 18-JUN-1999 11-FEB-1999.

Claim 34; Page 648; 675pp; English.

AAX40438 to AAX40715 represent 5' expressed sequence tags (ESTB) for human secreted proteins expressed in proseate, and encode the proteins given in AAY11716 to AAY11993 respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation and differentiation activity, haematopoiesis regulating

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and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                       Local Similarity
                                                 Sequence 78 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EP1033405-A2
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                                                                                      Query Match
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activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactis/chemokinetic activity, haemostatic and thrombolytic activity, receptor/ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptides can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were brepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences have been obtained, the full 5' UTR is rarely longer cDNA sequences have been obtained, the full 5' UTR is rarely therefore be used to obtain full langth cDNAs and genomic DNAs. SETS are also used to obtain full langth cDNAs and genomic DNAs. SETS are also used to obtain full langth cDNAs and genomic DNAs. SETS are also used to obtain full langth cDNAs and sendin diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                 1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                                                                                              1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                            86.8%; Score 402; DB 2; Length 79;
100.0%; Pred. No. 5.9e-40;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Giordano J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy; chromosome mapping
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Best Local Similarity 100.
Matches 79; Conservative
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                                                                                                                                                                                        Sequence 79 AA;
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                                               1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                                    1 MEHYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGS
                    Gaps
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Score 395; DB 3; Length 78;
Pred. No. 4e-39;
                  0; Indels
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         100.0%; Pred. No. 4e-
ive 0; Mismatches
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85.3%;
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                  78; Conservative
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9US-0147302P 9US-0147192P 9US-0147260P 9US-0147303P 9US-0147416P 9US-0147431P 9US-0148131P 9US-0148319P 9US-0146841P 9US-0146841P 9US-0149368P 9US-0149368P 9US-0149368P	990'S-0149723P 990'S-0149929P 990'S-0149930P 990'S-0150684P 990'S-01510684P 990'S-0151068P 990'S-0151060P 990'S-0151303P 990'S-0151303P 990'S-0151303P 990'S-015303P 990'S-015303P 990'S-015303P 990'S-015303P 990'S-015303P 990'S-015403P 990'S-015568P 990'S-015568P 990'S-015568P 990'S-015568P 990'S-0156458P	905-015/7519 905-015/7519 905-015/8659 905-0158239 905-01582939 905-01582939 905-01582939 905-01593319 905-015933109 905-015933109 905-015933109 905-015933109 905-015933109 905-015933109 905-015933109 905-015933109 905-015933109	9US-0160814 9US-0160815 9US-0160981 9US-0160981 9US-0161404 9US-0161405 9US-0161361 9US-0161361 9US-0161361 9US-0161361 9US-0161361 9US-0161923
4-AUG-1999 5-AUG-1999 5-AUG-1999 6-AUG-1999 6-AUG-1999 9-AUG-1999 9-AUG-1999 3-AUG-1999 3-AUG-1999 7-AUG-1999 6-AUG-1999	20-AUG-1999; 23-AUG-1999; 23-AUG-1999; 23-AUG-1999; 25-AUG-1999; 27-AUG-1999; 27-AUG-1999; 30-AUG-1999; 31-AU	6 - 0 - 1 - 1 - 1 - 2 - 2 - 2 - 2 - 2 - 2 - 2	11-0CT-1999 2-0CT-1999 2-0CT-1999 5-0CT-1999 5-0CT-1999 6-0CT-1999 6-0CT-1999 8-0CT-1999
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Ruben SM,
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                                                                                                                          14.5%;
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                                                                                                                                                                                                                                                                                                                                20-MAY-2004 (first entry)
                                                                                                                                     Best Local Similarity 41.0
Matches 16; Conservative
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SHI Y.
LAFLEUR D W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROSEN C A.
RUBEN S M.
DUAN D R.
  diabetes, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gastrointestinal
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Wei
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                                                                                                Sequence 70 AA;
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Lafleur DW,
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                                                                                                                          Query Match
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                                                                                                                                                                                                                                                 RESULT
88888888888
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The polynuclectide sequences given in AAA56346 to AAA26458 encode the human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins given in AAY91451 to AAY91691. The human secreted proteins can have activities based on the tissues and cells they are expressed in. Examples of the activities are: cytostatic; incurprotective; antialorgic; osteopathic; antiarthritic; antibacterial; antidiabetic; antialorgic; osteopathic; and cardiant. The polynucleotides and their corresponding secreted proteins are useful for preventing, treating or antialorating medical conditions, e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of mutations in the proteins in a sample or by determining the presence of the amount of the polynucleotides. Specific uses are described for each of the colling products for the diagnosis or treatment of concer, tumours, neurodegenerative disorders, developmental abnormalities and foctal deficiencies, blood disorders, diseases of the immune system, autoimmune diseases, hepatic and reand disease, inflammation, allergies, Alzheimer's and behavioural disorders, schizophrenia, osteoporosis, arthritis, infections, AIDS, spinal cord injuries, transplant rejection,
                                        ö
                                                                                                                                                                                                                                                                    Human; secreted protein; diagnosis; cytostatic; immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic; osteopathic; antiarthritic; antibacterial; antidabetic; antiasthma; antipsoriatic; cardiant; gene therapy; cancer; neurological disorder; immune disease; inflammation; blood disorder; tumour.
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated human genes and the secreted polypeptides they encode, useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders.
                                                                  87
                                                                                            55
                                                                                                                                                                                                                                             Human secreted protein sequence encoded by gene 94 SEQ ID NO:363.
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                                                                                3 RARNYITYAMALLXENKSNEVIFKAMGRAINKSVTIVELIKRRIPGLHQITSI
                                                            35 KIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAVSCAEIVKRRVPGLHQLTKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM, Duan R, Moore PA, Shi
e KA, Young PE, Brewer LA;
Olsen HS, Mucenski M;
        25.7%; Score 119; DB 3; Length 74; 39.6%; Pred. No. 3e-06; ive 12; Mismatches 20; Indels
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Lafleur_b, Wei Y, Ni J, Florence K
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                                                                                                                                                           AAY91690 standard; protein; 70 AA
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98US-0095486P.
98US-0095454P.
98US-0095455P.
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                                                                                                                                                                                                                 (first entry)
                                   Conservative
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Endress GA, E
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                     Similarity
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                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
        Query Match
Best Local Simil
Matches 21; C
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06-AUG-1998;
06-AUG-1998;
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antinflammatory; neuroprotective; nootropic; antiparkinsonian;
antianflammatory; neuroprotective; nootropic; antiarthritic;
antiasthmatic; anti-HIV; virucide; endocrine; cytostatic;
immunosuppressive; anti-HIV; virucide; endocrine; cytostatic;
immunosuppressive; antiallergic; cardiovascular; respiratory;
we dermatological; antimicrobial; gastrointestinal; gene therapy;
neurodegenerative disease; baravioral disorder; inflammatory condition;
hyperproliferative disorder; Alzahmer's disease; Parkinson's disease;
Wentington's disease; metabolic disorder; ray-sach's disease;
websh-Nyhan syndrome; reproductive disorder; immunological disorder;
arthritis; asthma; ALDS; endocrine disorder; immune disorder;
wedsh-Nyhan syndrome; haematopoletic disorder; muscular disorder;
welsemaia; autoimmune disorder; allergy; cancer; cardiovascular disorder;
respiratory disorder; pulmonary disorder; connective tissue disorder;
we skin disorder; CNS disorder; congenital disorder;
we skin disorder; CNS disorder; congenital disorder;
we skin disorder; CNS disorder; congenital disorder; infectious disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ï
                           reproductive disorders, gastrointestinal disorders, respiratory disorders and metabolic disorders. The proteins or polynucleotides can also be used as food additives or preservatives. The proteins are also useful for identifying their binding partners. AAA26337 to AAA26345 and AAA91450 are sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
sepsis, acne, psoriasis, cardiovascular disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Υ,
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                                                                                                                                                                                                                                                                                                                                                                                                Length 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 PAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGS
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                                                                                                                                                                                                                                                                                                                                                                                                Score 67; DB 3;
Pred. No. 4.5;
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Mismatches
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New nucleic acid molecules, useful in preparing a composition for treating or preventing e.g. inflammatory, CNS, bacterial or viral disorders, cancer, psoriasis, diabetes, ischemic heart disease or ulcerative colitis.
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                                                          15-NOV-2002; 2002US-0426394F.
15-NOV-2002; 2002US-0426394F.
27-NOV-2002; 2002US-0426394F.
27-NOV-2002; 2002US-0426316F.
27-NOV-2002; 2002US-0429302P.
27-NOV-2002; 2002US-0429302P.
27-NOV-2002; 2002US-0429651P.
04-DEC-2002; 2002US-0430654F.
04-DEC-2002; 2002US-0430651P.
04-DEC-2002; 2002US-0430651P.
04-DEC-2002; 2002US-0430651P.
04-DEC-2002; 2002US-0430651P.
04-DEC-2002; 2002US-0430651P.
04-DEC-2002; 2002US-0430651P.
04-DEC-2002; 2002US-0430661P.
04-DEC-2002; 2002US-0430651P.
05-DEC-2002; 2002US-0430651P.
05-DEC-2002; 2002US-0430661P.
06-DEC-2002; 2002US-043310P.
06-DEC-2002; 2003US-0460820P.
06-MAY-2003; 2003US-0467203P.
06-MAY-2003; 2003US-0467203P.
06-MAY-2003; 2003US-0467200P.
06-MAY-2003; 2003US-046720P.
06-MAY-2003; 2003US-046720P.
06-MAY-2003; 2003US-046720P.
06-MAY-200
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09-JUN-2003; 2003US-0476621P.
09-JUN-2003; 2003US-0476632P.
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08-JUL-2003; 2003US-04852I7P
08-JUL-2003; 2003US-04852I8P
08-JUL-2003; 2003US-048523P
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08-JUL-2003; 2003US-0485325P.
08-JUL-2003; 2003US-0485359P.
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Halenbeck RF, Kotnance.
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N-PSDB; ADN98580.
                        15-NOV-2002;
15-NOV-2002;
15-NOV-2002;
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    The invention describes an isolated human nucleic acid molecule (I)

comprising a polynucleotide having a nucleotide sequence at least 95%
identical to: a sequence polynucleotide fragment of SEQ ID NO: X or of
the cDNA sequence included in ATCC Deposit No: Z, which is hybridisable

to SEQ ID NO: X; or a sequence encoding a polypeptide fragment, domain or
comprising a biological activity. The nucleic acids and polypeptides,
plarmaccutical formulations and kits are useful in diagnosing and
treating neurodegenerative diseases states, behavioral disorders,
inflammatory conditions, hyperprolferative disorders (e.g. Alzheimer's
disease, Parkinson's disease or Huntington's diseases), metabolic
disorders (e.g. Tay-Sach's disease or Leash-Nyhan syndrome), reproductive
disorders (e.g. Tay-Sach's disease or Leash-Nyhan syndrome), reproductive
disorders (e.g. Tay-Sach's disease or Leash-Nyhan syndrome), haematopoietic
conductine and immunological disorders (e.g. Hodgkin's lymphoma), haematopoietic
conductine and immuno disorders (e.g. Hodgkin's lymphoma), haematopoietic
conductine affilicting connective tissue, skin disorders, allergy,
cancer, cardiovascular, respiratory or pulmonary disorders, allergy,
cancer, cardiovascular, respiratory or pulmonary disorders, allergy,
cancer, cardiovascular, respiratory or pulmonary disorders, allergy,
cancer, cardiovascular, nespiratory or pulmonary disorders, allergy,
cancer, cardiovascular, nespiratory or pulmonary disorders, conders,
conditions afflicting connective tissue, skin disorders fragment of the invention. Note: This sequence does not appear in
the printed specification but is available in electronic format from the
cut fragment of the invention. Note: This sequence does not appear in
the printed specification but is available in electronic format from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     anti-inflammatory; dermatological; neuroprotective; immunomodulator; antibacterial; vitucide; antipacriatic; grobe therapy; vaccine; inflammatory; CNS; immune disorder; cancer; psoriasis; diabetes; early aging; hormonal imbalance; ischemic heart disease;
                                      New human secreted nucleic acid, useful for diagnosing and treating
neurodegenerative, inflammatory, hyperproliferative, metabolic,
reproductive, cardiovascular, respiratory or immunological disorders or
diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14.5%; Score 67; DB 8; Length 70; 41.0%; Pred. No. 4.5;
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                                                                                                                                                Disclosure; SEQ ID NO 375; 234pp; English.
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25-OCT-2002; 2002US-04210B0P.
25-OCT-2002; 2002US-0421552P.
25-OCT-2002; 2002US-042117P.
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Matches 16; Conservative
WPI; 2004-180094/17.
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Hestir K, Beaurang PA, Behrens D;
 Lin H, Linnemann T, Pierce K, Wang Y;
 Zeng C;

4,

Gaps 54

17;

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The invention relates to a nucleic acid molecule comprising a polymucleotide sequence or its complement that encodes a polymetide. The nucleic acid is useful in preparing a composition for treating or preventing inflammatory, CNS, immune, bacterial or viral disorder, cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic heart disease or ulcerative colitis. This sequence corresponds to a protetin of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to the entire genome of cyanophage S-2L, and to the protein encoded by it. Genes isolated from the genome of S-2L are useful for preparing enzymes for synthesis of D-bases (D = 2,6-diaminopurine), particularly D, dDMP and dDTP, or polymcleotides containing these bases, polymerases involved in metabolism of D-bases and deoxynucleotide analogs, for chemotherapy of AIDS. The genes, and encoded polypeptides, and be used for detection and/or identification of S-2L, and for identifying agents that modulate synthesis of D-bases or polymucleotides containing them, and fusions of S-2L polypeptides with an antigen can be used to raise specific antibodies, useful for detecting S-2L. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New genomic sequence for cyanophage S-2L, useful for identifying genes for synthesis of 2,6-diaminopurine bases or polynucleotides containing
                                                                                                                                                                                                                                                                                                        7 AGSV--ELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEG----GSARH
                                                                                                                                                                                                                13.5%; Score 62.5; DB 8; Length 63; 40.7%; Pred. No. 14; ative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pochet S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genome; cyanophage; 2; 6-diaminopurine; chemotherapy; AIDS.
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Robert C, Vico V;
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(CNRS ) CNRS CENT NAT RECH SCI.
(GENO-) GENOSCOPE CENT NAT SEQUENCAGE GRP INTERE.
Claim 14; SEQ ID NO 964; 532pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cyanophage S-2L encoded protein #507.
                                                                                                                                                                                                                                                                                                                                                                                                           ADG22762 standard; protein; 84 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-APR-2002; 2002FR-00005424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-APR-2002; 2002FR-00005424.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-FEB-2004 (first entry)
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Weissenbach J, Saurin W,
                                                                                                                                                                                                                                 Local Similarity 40.7
1es 22; Conservative
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N-PSDB; ADG22255.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cyanophage S-2L
                                                                                                                                                                               Sequence 63 AA;
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Sequence 84 AA;

genome.

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                                                 12 AGOMVLPAPPGLGLDRGPLDEQEEQGVAMGVELPERVVPVAGVAGAGRLEQG-----PAG
                                    7 AGSVELPAP----SPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSG
                      Gape
                     16;
  Length 84;
                    26; Indels
                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 41968.
DB 8;
13.4%; Score 62; DB 29.3%; Pred. No. 22; ive 11; Mismatches
                                                                                                                                           AAG34486 standard; protein; 86 AA.
                                                                                                                                                                                                                                                                                                                                            99US-0123180P.
99US-0123548P.
99US-0125788P.
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99US-0131449P.
99US-0132048P.
99US-01324407P.
99US-0132484P.
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9905-01342189-
9905-0134219-
9905-0134370P-
9905-0134370P-
9905-0134370P-
9905-0135124P-
9905-0135124P-
9905-0135629P-
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99US-0130077P.
99US-0130449P.
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99US-0132487P.
99US-0132863P.
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99US-0136782P.
99US-0137222P.
99US-0137528P.
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                                                                          60 SGRAAGKAVSCAEIV 74
                                                                                       66 GGH---RAVTRREAV 77
                                                                                                                                                                                (first entry)
                    22; Conservative
                                                                                                                                                                                                                                                         Arabidopsis thaliana
Query Match
Best Local Similarity
Matches 22; Conserv
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04-7UN-1999)
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110-7UN-1999)
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22 - 70N - 1999;
23 - 70N - 1999;
24 - 70N - 1999;
26 - 70N - 1999;
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04-AUG-1999;
04-AUG-1999;
05-AUG-1999;
05-AUG-1999;
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0-JUN-1999;
1-JUL-1999;
1-JUL-1999;
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Length . . 8 61.5; D No. 26; Score Pred. 13.3%; 36.5%; Query Match Best Local Similarity

86;

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990S-0139456P.
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990S-0139460P.
990S-0139461P.
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990S-0139461P.
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990S-0145192P

990S-0145218P

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990S-0145919P

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99US-0142977P.
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990S-0145086P.
990S-0145088P.
  16 - JUN - 1999;
17 - JUN - 1999;
18 - JUN - 1999;
22 - JUN - 1999;
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11-AUG-1999;
12-AUG-1999;
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03-AUG-1999;
04-AUG-1999;
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19-JUL-1999
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   3
                                                                                                                                       Protein identification, signal transduction pathway, metabolic pathway, hybridisation assay, genetic mapping, gene expression control, promoter;
 4; Mismatches 18; Indels 11; Gaps
                14 APSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAG 65
                          Arabidopsis thaliana protein fragment SEQ ID NO: 75896.
                                                                        AAG58753 standard; protein; 71 AA
                                                                                                                                                                                                                                      99US-0121825P.
99US-012548P.
99US-012548P.
99US-012548P.
99US-012664P.
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99US-0126714P.
99US-0128734P.
99US-0128734P.
99US-0130077P.
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99US-0137502P.
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99US-0139119P.
99US-0139452P.
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                                                                                                       18-OCT-2000 (first entry)
19; Conservative
                                                                                                                                                        termination sequence
                                                                                                                                                                        Arabidopsis thaliana
                                                                                                                                                                                        EP1033405-A2
                                                                                                                                                                                                                                                                                                                                              23-APR-1999;
28-APR-1999;
30-APR-1999;
30-APR-1999;
04-MAY-1999;
06-MAY-1999;
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16-APR-1999;
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21-APR-1999;
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14-MAY-1999
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                                                                                        AAG58753;
Matches
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AAG58753
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 16390.
                                  AAG15942 standard; protein; 74 AA.
                                                                                                                                                                                                                                                                                                                                   9905-0121825P

9905-0123180P

9905-0123180P

9905-0125788P

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                                                                                           17-OCT-2000 (first entry)
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20-MAY-1999;
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10-JUN-1999;
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18-JUN-1999
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      RESULT 10
                     AAG15942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.4%; Score 57.5; DB 3; Length 71; 32.0%; Pred. No. 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Mismatches 12; Indels
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les 16; Conserv
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05-0CT-199
06-0CT-1999
07-0CT-1999;
8-0CT-1999;
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27-AUG-1999;
30-AUG-1999;
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15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
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23-SEP-19
24-SEP-19
28-SEP-19
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18-JUN-1999

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990S-0144332P.
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18 - JUN - 1999;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . Match 12.4%; Score 57.5; DB 3; Length 7 Local Similarity 32.0%; Pred. No. 66; les 16; Conservative 7; Mismatches 12; Indels
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Gaps

13-FEB-2002 (first entry)

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Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypethyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                               Human ORFX protein sequence SEQ ID NO:20790.
                                                                                                                                                                                                                                                                                                                    29-MAY-2001; 2001WO-US010836.
                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000; 2000US-0206132P.
29-AUG-2000; 2000US-0228716P.
                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-106308/14.
                                                                                                                                                                                          myasthenia gravis
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                                                                                                                                                                                                                                                      WO200192523-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                               Shimkets RA,
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                   36-DEC-2001.
                   24-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated polymucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymuclectides are also used in diagnostics as expressed sequence tags for identifying expressed cerivity of (II) as useful in gene therapy techniques to restore normal cerivity of (II) as useful in gene therapy techniques to restore normal useful for generating antibodies against it, detecting or quantitating a polypeptide in issue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic mino acid sequences of the invention. Note: The sequence data for this electronic format directly from WHO at capear in the printed specification, but was obtained in electronic format directly from WHO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 RKAGSVELPA--PSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 57.5; DE Pred. No. 77; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 20; SEQ ID NO 31086; 103pp; English.
            Novel human diagnostic protein #718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP10404 standard; protein; 75 AA.
                                                                                                                                                                                       30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.4%;
32.3%;
                                                                                                                                                                                                                  31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167,
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Best Local Similarity 32.3°
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                             WPI; 2001-639362/73.
N-PSDB; AAS64914.
                                                                                                                                                                                                                                                                                               Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 AAGKA 67
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                                                                                                                         WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 AAGKA
                                                                                            Homo sapiens.
                                                                                                                                                        11-OCT-2001
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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABM15762 to ABM27252 encode the human ORFX in the specification). ABM15762 to ABM27252 encode the human ORFX proteins given in ABP00101 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder. ORFX polynucleotide content associated in the manufacture of a medicament for treating a squances can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage, costeoarthritis, neurodegenerative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders related to organ transplantation, cardiovascular diseases, disorders, infectious costeoarthritis, autoimmune disorders, hypothyroidism, cholesterol ester storage disease, various immune deficiencies and disorders, infectious diseases, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host diseases and autoimmune inflammatory eye disease. ORFX proteins are also cuseful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from protection or regeneration stissues and conditions resulting from cyctokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic cycromated dispersed in the printed specification, int/publypublished_pot_essequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12; Indels
Disclosure, SEQ ID NO 20790; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
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AAG64347

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a peptide encoded by a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 GSVELP-----APSPMPQLPPDTLEMRVRDGSKIR-----NLLGLALGRLE 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 27; SEQ ID NO 35675; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.6%; Score 53.5; DB 4; Length 67; 30.8%; Pred. No. 1.7e+02; ive 8; Mismatches 11; Indels ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide #10907 encoded by probe for measuring placental
                                                                                                                                                                                                                                                                                                        Chen W, Rank DR;
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                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM36870 standard; protein; 67
                                                                                                                                                        30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-0.632366.
21-SEP-2000; 2000US-0.234687P.
27-SEP-2000; 2000US-0.236359P.
                                                                                     30-JAN-2001; 2001WO-US000669
                                                                                                                                                                                                                                 04-OCT-2000; 2000GB-00024263
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30-UUN-2000; 2000US-00608408
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0236359P.
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                                                                                                                                                                                                                                                                                                      Penn SG, Hanzel DK,
                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483447/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 67 AA;
             WO200157277-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200157272-A2
                                                                                                                       04-FEB-2000;
26-MAY-2000;
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                                                  09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOD protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a novel protein: Copper/Zinc (Cu/Zn) SOD protein family 9. The protein and its coding sequence are useful for the diagnosis and treatment of malignant tumour, haemopathy, HIV infection, immunological diseases and various inflammations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------LGLFLFLLHGGASR-----GAGH---RSLTCP
                                                                                                                                                                                    Cu/Zn SOD protein, copper/zinc SOD protein; cytostatic; haemostatic; virucide; immunomodulatory; antiinflammatory; gene therapy; malignant tumour; haemopathy; HIV infection; immunological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; foetal liver; gene expression; single exon nucleic acid probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide #10546 encoded by human foetal liver single exon probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copper/zinc SOD protein family 9 and encoded polynucleotide, u diagnosis and treatment of malignant tumors, hemopathy, human immunodeficiency virus infection, immunological diseases and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 83;
2e+02;
ches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.7%; Score 54; 25.4%; Pred. No.
                                          AAG64347 standard; protein; 83 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 28; 32pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                      25-DEC-2000; 2000WO-CN000676.
                                                                                                                                                                                                                                                                                                                                                                                                                         99CN-00125785
                                                                                                                                                     Cu/Zn SOD protein family 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 11.7%
Best Local Similarity 25.4%
Matches 16; Conservative
                                                                                                                 (first entry)
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N-PSDB; AAH49688.
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                                                                                                                                                                                                                                                                                                               WO200147996-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xie Y;
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inflammation
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                                                                                                                 25-SEP-2001
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Mao Y,

<u>ب</u>

Gaps

17;

gene expression.

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ABB43040;

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ABB43040

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Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human placenta.
                                                                                             Claim 27; SEQ ID NO 37139; 654pp; English.
                                   Chen W, Rank DR;
                  (MOLE-) MOLECULAR DYNAMICS INC.
04-OCT-2000; 2000GB-00024263.
                                   Hanzel DK,
                                                  WPI; 2001-488897/53.
                                   Penn SG,
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The present invention relates to single exon nucleic acid probes (SENP: see AAI31315-AAI57546). The present sequence is a peptide encoded by one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders Sequence 67 AA;

11; Indels 17; Gaps Query Match 11.6%; Score 53.5; DB 4; Length 67; Best Local Similarity 30.8%; Pred. No. 1.7e+02; Matches 16; Conservative 8; Mismatches 11; Indels 1

3;

ò a Search completed: January 26, 2005, 15:31:21 Job time : 160 secs

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January 26, 2005, 15:34:56 ; Search time 143 Seconds (without alignments) 229.911 Million cell updates/sec
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1 MEHYRKAGSVELPAPSPMPQ.......BIVKRVPGLHQLTKLRFLQ 91
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1: \cgn2 \( \) \cgn\( \) \c
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                                                                                                                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	E	Sequence 237341,	186121,	375, App	"	141539,		33700, A	35766, A	259300,		362864,	147885,	113150,
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence
	αı	US-10-425-115-237341	US-10-424-599-186121	US-10-351-334-375	US-10-425-115-240946	US-10-437-963-141539	US-10-437-963-135348	US-10-767-701-33700	US-10-767-701-35766	US-10-425-115-259300	US-10-425-115-333500	US-10-425-115-362864	US-10-437-963-147885	US-10-437-963-113150
		17	15	15	17	16	16	16	16	17	17	17	16	16
	Query Match Length DB	72	87	70	79	81	75	91	86	80	87	61	98	87
ф	Query	62.9	14.7	14.5	14.4	13.3	13.1	13.0	12.6	12.4	12.4	12.3	12.3	12.3
	Score	305	68	67	66.5	61.5	60.5	9	58.5	57.5	57.5	57	57	57
	Result No.	7	7	Э	4	S	y	7	80	6	10	11	12	13

	Sequence 251264, Sequence 359657, Sequence 39398, A Sequence 197142, Sequence 159456, Sequence 294016.		Sequence 165120, Sequence 165120, Sequence 16182, Sequence 197812, Sequence 260434, Sequence 170394,	Sequence 4719, Ap Sequence 173391, Sequence 180208, Sequence 173227, Sequence 173227, Sequence 271602, Sequence 31999, A Sequence 319753,
-10-424-599-19083 -10-437-963-10787 -10-437-963-14110 -10-425-115-22136	-425-11 -425-11 -767-70 -425-11 -437-96	10-864-76 -10-425-1 -10-437-9 -10-425-1 -10-425-1	-425-115-36652 -437-963-16512 -437-963-16188 -437-963-19781 -425-115-26043	10-106-69 10-437-96 10-437-96 10-437-96 10-437-96 10-425-11 10-029-38
15 16 17 17		9 11 11 17 17	110	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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ALIGNMENTS

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Sequence 237341, Application US/10425115
| Publication No. US20040214272A1
| General Information:
| General Information:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Kovalic, David K.
| APPLICANT: Town, Yihua
| APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
| TITLE OF INVENTION: Numbers US/10/425,115
| CURRENT APPLICATION NUMBER: US/10/425,115
| CURRENT PILING DATE: 2003-04-28
| NUMBER OF SEQ ID NOS: 369326
| SEQ ID NO 237341
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US-10-425-115-237341
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Best Local Similarity
Matches 62; Conservat
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US-10-437-963-141539

US-10-437-963-141539

Sequence 141539, Application US/10437963

Fublication No. US20040123343A1

GENERAL INFORMATION:

APPLICANT: Exemply Royal R.

APPLICANT: Cao, Yongwei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21 (53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 141539

LENGTH: BL
                                                                                                                                                                                                                          Sequence 240346, Application US/10425115
Sequence 240346, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Abou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (53222)8
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
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                                                                10 PLPSPAPALAP-----AHSLLGLLLGRMSGSS 36
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US-10-437-963-141539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: MRT4577_151321C.1.pep
US-10-425-115-240946
                      13 PAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGS
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13.3%; Score 61.5; DB 16;
Best Local Similarity 38.3%; Pred. No. 48;
Matches 23; Conservative 6; Mismatches 22;
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57 FLPLKRGTIFGIH 69
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ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Zea mays
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                   Sequence 186121, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La ROSA Thomas J
APPLICANT: La ROSA Thomas J
APPLICANT: About Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US, 110/424, 599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 186121
LENGTH: 87
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Best Local Similarity 27.8%; Pred. No. 10;
Matches 20; Conservative 12; Mismatches 26; Indels
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14.5%; Score 67; DB 15; Length 70;
Best Local Similarity 41.0%; Pred. No. 10;
Matches 16; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_13907C.1.pep
US-10-424-599-186121
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APPLICANT: Konacteoulis

TITLE OF INVENTION: 98 Human Secreted Proteins
FILE REFERENCE: PZ031P2

CURRENT APPLICATION NUMBER: US/10/351,334

CURRENT PILING DATE: 2003-01-27

PRIOR PILING DATE: 2003-01-27

PRIOR PILING DATE: 2000-01-24

PRIOR PILING DATE: 2000-01-24

PRIOR PILING DATE: 1998-07-29

PRIOR PILING DATE: 1998-07-30

PRIOR PILING DATE: 1998-07-30

PRIOR PILING DATE: 1998-08-05

PRIOR PILING DATE: 1998-08-05

PRIOR PILING DATE: 1998-08-05

PRIOR PILING DATE: 1998-08-12

PRIOR PILING DATE: 1998-08-12

PRIOR PILING DATE: 1998-08-15

PRIOR PILING DATE: 1998-08-06

PRIOR PILING DATE: 1998-08-06
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Publication No. US20040034196A1
GENERAL INFORMATION:
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67 RKIEGTGTLSGR 78
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US-10-424-599-186121
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Gaps

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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 259300
LENGTH: 80
                                                                                                                                                       US-10-767-701-35766

Sequence 35766, Application US/10767701

Publication No. US20040172684A1

Publication No. US20040172684A1

Publication No. US20040172684A1

APPLICANT: Cao. Vordence

APPLICANT: Cao. Yongel

APPLICANT: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 VELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAVS 69
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12.6%; Score 58.5; DB 16; Length 86;
Best Local Similarity 32.8%; Pred. No. 1.18+02;
Matches 19; Conservative 5; Mismatches 25; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C74430_1.pep
US-10-767-701-35766
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 333500, Application US/10425115
    35 AGAVEAPAAPPAPRRPPGTRRTR 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | :: | :: | ... | 49 CHDLGDSGARRADRVSKLPYGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 23.28 Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
US-10-425-115-333500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 35766
LENGTH: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharzov, Andrey A.
APPLICANT: Bucharzov, Andrey A.
APPLICANT: Li, Ping
APPLICA
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Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(51535)B
CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 33700
LENGTH: 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DTLEMRVRDGS-----KIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAVSCAEIVKRRV 78
                                                                                   DPLERRIWEGSFEAAAARRRAGLAGGRALGGLAPNV--GRGGRGAGRCYWI--LIKRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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13.1%; Score 60.5; DB 16; Length 75;
Best Local Similarity 31.5%; Pred. No. 57;
Matches 23; Conservative 12; Mismatches 27; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.0%; Score 60; DB 16; Length 91; 52.2%; Pred. No. 82; tive 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Clone ID: SORBI-28MAY03-C35716_1.pep
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CTHER INFORMATION: Clone ID: PAT_MRT4530_37033C.1.pep

US-10-437-963-135348
                                                                                                                                                                                                                                                                                                                         Sequence 135348, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 AGSVELPAPSPMPQLPPDTLEMR 29
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Best Local Similarity 52.29
Matches 12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                             -10-437-963-135348
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LENGTH: 75
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APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.

APPLICANT: Barbazuk, Brad

APPLICANT: Li, Ping

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

CURRENT APPLICATION NUMBER: US/10/437,963

NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 147885

TYPE

THE BETT APPLICATION NUMBER: US/10/437,963

THE BETT APPLICATION NUMBER: US/10/437,963

THE BETT APPLICATION NUMBER OF SEQ ID NOS: 204966

THENGTH: 86
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; Sequence 113150, Application US/10437963
; Publication No. US20040123343A1
; RENEMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zoo, Yongwei
; APPLICANT: Aco, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Wu, Wei
; APPLICANT: Wu wei
; APPLICANT: Wi, Public Main and Uses Thereof for Plant Improvement
; APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: 12, 153221)
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 113150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_48370C.1.pep
US-10-437-963-147885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Clone ID: PAT_MRT4530_16966C.1.pep
US-10-437-963-113150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
12.3%; Score 57; DB 16; L
Best Local Similarity 45.7%; Pred. No. 1.6e+02;
Matches 16; Conservative 4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45 GRL--EGGSARHVVFSGSGRAAGKAVSCAEIVKRR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 GRLGGEGGQARNGAASGLGRDAGYRMERGEVDGRQ 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.3%; Score 57; DB 16; 32.2%; Pred. No. 1.7e+02; ive 3; Mismatches 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)..(87)
OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity 32.2'
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Oryza sativa
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NAME/KEY: unsure
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               GENERAL INFORMATION

APPLICANT: La Rosa, Thomas J.

APPLICANT: AROUTE, Vidua

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

APPLICANT: Co., Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: NUCLEIC ACID

TITLE OF INVENTION: NUCLEIC ACID

TITLE OF INVENTION: NUCLEIC ACID

TITLE OF INVENTION: APPLICATION NUMBER: US/10/425,115

CURRENT APPLICATION NUMBER: 2003-04-28

SEQ ID NOS: 369326

LENGTH: 87
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Bublication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thous
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICANTION: Plants
FILE REFERENCE: 2023-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 362864
LENGTH: 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 APSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAVSCAEI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----ALEVGPCRH-----GPASSRAVPCLGT 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 57.5; DB 17; Length 87;
Pred. No. 1.5e+02;
9; Mismatches 18; Indels 1!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
12.3%; Score 57; DB 17; Length 61;
Best Local Similarity 30.3%; Pred. No. 1.1e+02;
Matches 20; Conservative 2; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       ) OTHER INFORMATION: Clone ID: MRT4577_67265C.1.pep
US-10-425-115-333500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: MRT4577_94106C.1.pep
US-10-425-115-362864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.4%;
Publication No. US20040214272A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 34.4*
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 AGPPCPTLGPST---
                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 VKRRVP 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 GSAR 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEER 82
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US-10-437-963-147885
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APPLICANT: La Roia, Thomas J.
APPLICANT: La Roia, Thomas J.
APPLICANT: Coo, Yibua
APPLICANT: Coo, Yongwei
APPLICANT: Coo, Yongwei
APPLICANT: Wi, Wei
APPLICANT: Buckharov, Andrey A.
APPLICANT: Buckharov, Andrey A.
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 107873
LENGTH: 91
                                                                             APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: En Rosa Thomas J
APPLICANT: About K
APPLICANT: About Vibra
APPLICANT: About Vibra
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)8
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 190837
LENGTH: 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PRPRPILTHMQPPSYXQCYQWRIAKHGGRPKFHHINTRHCALLRXHGGPPLHIVYGWVGK 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 12.1%; Score 56; DB 15; Length 90; Best Local Similarity 27.1%; Pred. No. 2.2e+02; Matches 19; Conservative 10; Mismatches 29; Indels 12; Gaps
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Pred. No. 2.3e+02;
4; Mismatches 15; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT3847_14345C.1.pep
US-10-424-599-190837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: PAT_MRT4530_12182C.1.pep
US-10-437-963-107873
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Glycine max
PEATURE:
NAME/KE:
LOCATION: (1)..(90)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (1)..(91)
OTHER INFORMATION: unsure at all Xaa locations
Sequence 190837, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-437-963-107873
; Sequence 107873, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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Best Local Similarity 37.0%;
Matches 17; Conservative
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ORGANISM: Oryza sativa
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NAME/KEY: unsure
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Search completed: January 26, 2005, 15:47:04 Job time : 145 secs

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Sequence 375, Application US/09489847

Patent No. 6476195

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FILE REPERENCE: P2031P1

CURRENT FILING DATE: 2000-01-24

EARLIER APPLICATION NUMBER: PCT/US99/17130

SARLIER APPLICATION NUMBER: PCT/US99/17130

SARLIER APPLICATION NUMBER: 60/094,657

EARLIER APPLICATION NUMBER: 60/094,657
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Best Local Similarity 100..

Best Local Similarity 100..
   6611
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ORGANISM: Homo sapiens
 US-09-513-999C-7680
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US-09-489-847-375
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Sequence 6159, Ap
Sequence 6159, Ap
Sequence 8, Appli
Sequence 1391, A
Sequence 1379, A
Sequence 37, Appl
Sequence 37, Appl
Sequence 329, A
Sequence 2841, A
Sequence 2841, A
Sequence 52617, A
Sequence 52610, A
Sequence 62, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 63, Appl
Sequence 64, Appl
Sequence 65, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 65, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 64, Appl
Sequence 65, Appl
Sequence 64, Appl
Sequence 66, Appl
                                                                                                      January 26, 2005, 15:24:36; Search time 38 Seconds (without alignments) 158.814 Million cell updates/sec
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Sequence 507
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Patent No.
                                                                                                                                                                                                   1 MEHYRKAGSVELPAPSPMPQ.....EIVKRRVPGLHQLTKLRFLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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(/GGIZ_6/fptddata1/iaa/5A_COMB.pep:*

(/GGIZ_6/fptddata1/liaa/6A_COMB.pep:*

(/GGIZ_6/fptddata1/liaa/6A_COMB.pep:*

(/GGIZ_6/fptddata1/liaa/6B_COMB.pep:*

(/GGIZ_6/fptddata1/liaa/PCTUS_COMB.pep:*

(/GGIZ_6/fptddata1/liaa/PCTUS_COMB.pep:*

(/GGIZ_6/fptddata1/liaa/backfiles1.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-513-999C-7680

US-09-489-647-375

US-09-511-6718-6

US-09-430-564-8

US-09-430-564-14

US-09-430-564-14

US-09-248-796A-1579

US-09-248-796A-13911

US-09-212-962-37

US-09-912-962-37

US-09-912-962-37

US-09-134-001C-2843

US-09-513-99C-6477

US-09-570-767-52630

US-09-570-767-52630

US-09-513-999C-6225

US-09-513-999C-6225

US-09-513-999C-6225

US-09-513-999C-6225

US-09-513-999C-6225

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US-09-134-000C-3428
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US-08-469-260A-507
US-08-488-446-507
US-08-467-344A-507
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                                                                                                                                                                                                                                                                                     478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                            - protein search, using sw model
                                                                                                                                                                  US-10-057-813-14_COPY_1_91
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Match Length
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49.5
49.5
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Maximum DB 8
                                                                            OM protein
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Sequence 7680, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961

FILE REPRENCE: 59. US2. RE
CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 1999-0.254

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR PILING DATE: 1999-0.26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 7680
                                               88, Appl
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                                               Sequence 8
Patent No.
Sequence 6
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Sequence
Sequence
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100.0%; Pred. No. 5.1e-42;
tive 0; Mismatches 0; Indels
ALIGNMENTS
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; Sequence 14, Application US/09430564;
; Patent No. 6372467;
; Barent No. 6372467;
; APPLICANT: John Blenis
; APPLICANT: Azivin Slenis
; APPLICANT: Azivin Slenis
; TITLE OF INVENTION: P5456K AND P8556K GENES, PROTEINS,
; TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
; TITLE OF INVENTION: PRIMERS, PROBES, AND DETECTION METHODS
; CURRENT APPLICATION NUMBER: US/09/430,564
; CURRENT FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/106,141
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FRAELSCQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 49.5; DB 3; Length 85;
Pred. No. 1.1e+02;
6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                  44 LGRLEGGSARHVVFSGSGRAAGKAVSCAEIVKR---RVPGLHQLTKLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 EHYRKAGSV----ELPAPSPMPQLPPDT---LEMRVRDGSK 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | :| : |: |: |: |: | | | 34 EGRRPSPSLPEPTELPLPDLPPLPPPSSTTAPLPIRPPSGTK 74
                                                                                                                                                                                                                                                  Query Match
10.9%; Score 50.5; D
Best Local Similarity 35.4%; Pred. No. 76;
Matches 17; Conservative 7; Mismatches
                                                                                        NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 81
              PRIOR APPLICATION NUMBER: 60/155,934
PRIOR FILING DATE: 1999-01-14
PRIOR APPLICATION NUMBER: 60/095,938
PRIOR FILING DATE: 1998-08-10
                                                                                                                                                                                           ORGANISM: Arabidopsis thaliana US-09-371-6718-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.7%;
36.6%;
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US-09-430-564-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 6
US-09-430-564-14
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LENGTH: 85
                                                                                                                                                                            TYPE: PRT
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LENGTH: 85
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Patent No. 6548743
Patent No. 6548743
Patent No. 6548743
TITLE OF INVENTION:
TITLE OF INVENTION: TRANSGENIC PLANTS EXPRESSING A
TITLE OF INVENTION: UDAL-SPECIFICITY MAPK PHOSPHATASE AND USES THEREOF
FILE REFERENCE: 00786/370002
CURRENT APPLICATION NUMBER: US/09/371,671B
CURRENT FILING DATE: 1999-08-10
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                                                                                                                                                                                                                                                                                                                      ch 14.5%; Score 67; DB 4; Length 70; l Similarity 41.0%; Pred. No. 0.54; 16; Conservative 2; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.2%; Score 52; DB 4; Length 69; 31.2%; Pred. No. 40; 22; Indels:ive 5; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 HYRKAGSVELPAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGG
                                                                                                                                                                                                                                                                                                                                                                                                13 PAPSPMPQLPPDTLEMRVRDGSKIRNLLGLALGRLEGGS 51
                                                                                                                                                                                                                                                                                                                                                                                                                                       10 PLPSPAPALAP-----AHSLIGLLIGRMSGSS 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Jobert, S.

APPLICANT: Glochert, S.

TITLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT APPLICATION NUMBER: US/09/621,976

SUFFRENCE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm
                    ; OTHER INFORMATION: Xaa = Cys, Gly, Arg, Ser
US-09-621-976-6159
EARLIER APPLICATION NUMBER: 60/095,486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-09-621-976-6159
Sequence 6159, Application US/09621976
Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 29
OTHER INFORMATION: Xaa = Ala, Pro
NAME/KEY: UNSURE
LOCATION: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.2
Best Local Similarity 31.2
Matches 15; Conservative
                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
US-09-489-847-375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 6159
LENGTH: 69
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US-09-371-671B-6
                                                                                                                                                                                                 SEQ ID NO 375
LENGTH: 70
                                                                                                                                                                                                                                          TYPE: PRT
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TITLE OF INVENTION: TELOMERE REPEAT BINDING FACTOR AND
DIAGNOSTIC AND THERAPEUTIC USE THEREOF
                                                                                                                                                                      APPLICANT: de Lange, Titia
APPLICANT: de Lange, Titia
APPLICANT: Broccoli, Dominique
APPLICANT: Broccoli, Dominique
APPLICANT: Broccoli, Dominique
TITLE OF INVENTION: TELCMERE REPEAT BINDING FACTOR AND
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USE THEREOF
NUMBER OF SEQUENCES: 52
CORRESPONDEM ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
STREET: 411 Hackenback Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/018,635
3 LPAPTDMSR---EALINRITNETKIOIALNLDGGKLE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 GGSARHVVFSGSGRAAGKAVSCAEIVKRR----VPGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10.4%; Score 48; DB
ilarity 44.4%; Pred. No. 73;
Conservative 3; Mismatches
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ADDRESSEE: KLAUBER & JACKSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: de Lange, Titia
Broccoli, Dominique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 37, Application US/09912962 Patent No. 6586577 GENERAL INFORMATION:
                                                                                                             ; Sequence 37, Application US/09018635; Patent No. 6297356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: David A. Jackson
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-:
TELECHONE: 201-487-5800
TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 amino acida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                    Hackensack
: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 16; Conserv
                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                  RESULT 9
US-09-018-635-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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Batent No. 6747137

GENERAL INFORMATION:

BAPLICAMY: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-113

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT PILING DATE: 1999-02-12

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

SEQ ID NO 16579

LENGTH: 87
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US-09-248-796A-16579
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29
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Pred. No. 1.5e+02;
8; Mismatches 12; Indels
                                                                    Length 85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.6%; Score 49; DB 4; Length 86; 37.9%; Pred. No. 1.3e+02;
                                                                                                               13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Indels
                                                                                                                                                                                         | :| : |: | : | : | | | 34 EGFRPSPSLPEPTLPLPPPLLPPPPPSSTTAPLPIRPPSGTK 74
                                                                                                                                                          2 EHYRKAGSV----ELPAPSPMPQLPPDT---LEMRVRDGSK 35
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                                                                  Score 49.5; DB 3;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 PAPSPMPQLPPD----TLEMRVRDGSKIR 37
                                                                                                                                                                                                                                                                                                               Sequence 13911, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.5%;
ilarity 37.8%;
Conservative
                                                                Query Match 10.7%;
Best Local Similarity 36.6%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13911
LENGTH: 86
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ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 37.99
Matches 11; Conservative
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                                                                               -09-489-039A-13911
       ; UKGANISM: HOT
US-09-430-564-14
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Sequence 2843, Application US/09134001C

Sequence 2843, Application US/09134001C

Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

FILE REFERENCE: GTC-07

CURRENT APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                             APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF THE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PATENTIN Ver. 2.0
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Batent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Glordano, J.Y.
TITLE OP INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US.2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 TLEMRVRDGSKIRNLLGLALGRLEGGSARHVVFSGSGRAAGKAVSCAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 71;
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10.4%; Score 48; DB 4; I
Best Local Similarity 27.1%; Pred. No. 1.3e+02;
Matches 13; Conservative 10; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                      ; Sequence 58217, Application US/09270767; Patent No. 6703491; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-58217
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Matches 15, Conserv
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                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 58217
LENGTH: 71
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Patent No. 6673910

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 3294
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0
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENT Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/912,962
FILING DATE: 25-Jul-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION: <UNKnown>
PRIOR APPLICATION: <UNKnown>
PRIOR APPLICATION: <UNKnown>
PRIOR APPLICATION: <UNKnown>
APPLICATION NUMBER: 09/018,635
FILING DATE: 04-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: DAVIA A. JGCKBOIN
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-142 CIP1
TELECOMMUNICATION INFORMATION:
MERTERENCE/DOCKET NUMBER: 600-1-142 CIP1
TELECOMMUNICATION INFORMATION:
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Pred. No. 1.1e+02;
9; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.4%; Score 48; DB 4; Length 45; 44.4%; Pred. No. 73; cive 3; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 201-487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acidd
TYPE: amino acid
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29.3%;
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MOLECULE TYPE: protein
DESCRIPTION: TRF2
                                               STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 44.41
Matches 16; Conservative
                          CITY: Hackensack
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Best Local Similarity 29.3
Matches 12; Conservative
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; ORGANISM: M.catarrhalis
US-09-540-236-3294
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US-09-270-767-37413
Sequence 37413, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFRENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 37413
LENGTH: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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10.2%; Score 47; DB 4; Length 59;
Best Local Similarity 47.4%; Pred. No. 1.4e+02;
Matches 9; Conservative 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 31.7%; Pred. No. 1.4e+02;
Matches 13; Conservative 6; Mismatches 14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-37413
; PRIOR APPLICATION NUMBER: US 60/122,487; PRIOR FILING DATE: 1999-02-26; NUMBER OF SEQ ID NOS: 36681; SOFWARE: Patent.pm; SEQ ID NO 6477; LEWGTH: S9; TYPE: PRT; ORGANISM: Homo sapiens US-09-513-999C-6477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: January 26, 2005, 15:36:08
Job time : 39 secs
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ORGANISM: Drosophila melanogaster
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38 RRPGQRRPPPPPPPPP 56
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                                                            January 26, 2005, 14:52:01; Search time 8.2 Seconds (without alignments) 481.084 Million cell updates/sec
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220
1 TKLRFLQTEDSWVPASPDTG......DPLTVRRHVPAVWVLLSRDP
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5.1.6
Compugen Ltd.
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                                                                                                                                                                                   283416 seqs, 96216763 residues
GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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T29237
AF3517
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JH0329
C38252
F70607
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seq length: 200000000
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Match Length DB
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39938
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Perfect score:
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53
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ALIGNMENTS	ALIGNMENTS ESULT 1 D0332 robable membrane protein YPO2724 [imported] - Yersinia pestis (strain C092)	45	20	22.7	-	~	T43916	chitinase A [impor
	ESULT 1 D0332 Conside membrane protein YP02724 [imported] - Yersinia pestis (strain C092)						ALIGNMENTS	
		robable m	embran	e pro	tein YP	0272	4 [imported] - Yer	einia pestis (strain CO92)
Arouss. Probable membrane protein YPO2724 [imported] - Yersinia pestis (strain CO92)	C.Species: reisimia pescis C.Date: 02-Nov-2001 #secmence revision 02-Nov-2001 #fext change 09-Jul-2004	Date: 02	-Nov-2	11.00 001 #	Sects	r.	vision 02-Nov-2001	#text change 09-Jil-2004

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R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AD0332
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1275 < KUR>
A;Residues: 1-1275 < KUR>
C;Genetics:
C;Genetics:
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29237
R;Cattung, S.; Mu, X.
submitted to the EMBL Data Library, November 1995
A;Pescription: The sequence of C. elegans cosmid F56E3.
A;Reference number: Z20592
A;Reference number: Z20592
A;Accession: T29237
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-1576 cGMT>
A;Residues: 1-1576 cGMT>
A;Cross-references: UNIPROT: Q81G10; EMBL: U41536; PIDN:AAB52613.1; GSPDB:GN00028; CESP:F
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A;Introns: 23/1; 47/2; 125/3; 162/2; 191/3; 274/2; 296/3; 498/3; 532/1; 651/3; 723/2; 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                30.2%; Score 66.5; DB 2; Length 1275; 47.1%; Pred. No. 2.2; ive 6; Mismatches 11; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 57; DB 2; Length 1576;
Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         806 LMLLQEEDRWVMAQSLSSSLDPLTLRQDVLVMYL 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LRFLOTEDSWVPA-SPDTGLDPLTVRRHVPAVWV 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Genetics:
A;Gene: CESP:F56E3.3
                                                                                                                                                                                                                                                                                                                                                                                           A; Gene: YPO2724
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T42761
R;Dieck, S:; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex,, J. Cell Baloi. 142, 499-509, 1998
A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localize.
A;Reference number: Z22249; MUID:98345363; PMID:9679147
A;Accession: T42761
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                A,Reaidues: 1-3938 -DIE>
A,Cross-references: UNIPROT:088778; EMBL:Y16563; NID:g3413503; PIDN:CAA76287.1; PID:g341
A,Experimental source: strain Sprague Dawley; brain
                                                                                                                                                                                                                                                                                                                                                                                         A)Description: may be involved in cytomatrix organization at the site of neurotransmitter A;Note: component of the presynaptic cytoskeleton C;Keywords: coiled coil; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Residues: 1-3942 <DIE>
A,Residues: 1-3942 <DIE>
A,Cross-references: UNIPROT:088737; EMBL:Y17034; NID:g3413809; PIDN:CAA76598.1; PID:g341
A,Experimental source: strain 129 SVJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Description: may be involved in cytomatrix organization at the site of neurotransmitte
A;Note: component of the presynaptic cytoskeleton
C;Keywords: coiled coil; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T42730
R;Dieck, S.; Sanmarti-Vila, L.; Langnaese, K.; Richter, K.; Kindler, S.; Soyke, A.; Wex,, Cell Biol. 142, 499-509, 1998
A;Title: Bassoon, a novel zinc-finger CAG/Glutamine-repeat protein selectively localizer A;Accession: T42730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog, A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: 9F1
A;Introns: 72/2; 208/3; 505/3; 675/3; 2889/3; 3582/1; 3851/3; 3886/1; 3930/1
A;Note: bassoon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bassoon protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 LOTEDSW-----VP----ASPDTGLDPLTVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 LOTEDSW------VP----ASPDTGLDPLTVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 54.5; DB 2;
Pred. No. 2.8e+02;
4; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 24.8%; Score 54.5; DB 2;
Best Local Similarity 35.0%; Pred. No. 2.8e+02;
Matches 14; Conservative 4; Mismatches 5;

    Caenorhabditis elegans

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A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              elegans Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 24.8%;
Local Similarity 35.0%;
les 14; Conservative
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Science 282, 2012-2018, 1998
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Matches
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PRESIDUES: 1-160 «KUR»
Cross-references: UNIPROT:Q8YDWO; UNIPROT:Q8FXN6; GB.AE008918; PIDN:AAL53305.1; PID:g1
                                                                                                                                                                                                                                                                                                                                      Ribelvecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letese Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Retession: AF3517
A;Status: preliminary
A;Residues: 1-160 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: G75578
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Rocatus: preliminary
A;Nolecule type: DNA
A;Residues: 1-785 <WHI>
A;Cross-references: UNIPROT:09RYQ4; GB:AE001863; GB:AE001825; NID:g6460670; PIDN:AAF1238
C;Genetics:
A;Genetics:
A;Gene: DRA0255
A;Map position: 2
                                                                                                                                                                                                                                      lactoylglutathione lyase (EC 4.4.1.5) [imported] - Brucella melitensis (strain 16M) c.fspecides: Brucella melitensis
C.fspecides: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
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Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
              Gaps
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              Indels
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        13;
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                                                                                 8 TEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRD 40
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        Mismatches
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Pred. No. 4.5;
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Pred. No. 40;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
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Best Local Similarity 44.4%;
Matches 12; Conservative
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ilarity 47.8%;
Conservative
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C,Genetics:
A,Genet BMEI10064
A,Map posttion: II
C;Keywords: carbon-sulfur lyase
11; Conservative
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Matches 11; Conserv
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Matches
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A; Accession: AB3562
A; Status: preliminary
A; Molecule type: DNA
A; Residuae: 1-608 < KUR>
A; Cross-references: UNIPROT: QBYCV9; GB: AE008918; PIDN: AAL53661.1; PID: g17984580; GSPDB: A; Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                      A;Gene: BWEI10419
A;Map position: II
C;Superfamily: GTP-binding membrane protein lepA; translation elongation factor Tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      167 NGWMALSPEGPKDQGLAPLFDLVLKHVPAPKVAEGPFRMIGTILEADP 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 24.1%; Score 53; DB 2; Length 608; Best Local Similarity 33.3%; Pred. No. 56; Matches 16; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 DSWVPASP----UTGLDPL--TVRRHVPA-----VWVLLSRDP
    A; Reference number: AD3252; PMID:11756688
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A;Status: preliminary
A;Molecule type: DNA
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Cipate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cipate: 05-Dec-1997 #text_change 05-Jul-2004
Cipate: 05-Dec-1997 #text_change 05-Dec-1997 #text_change 05-Jul-2004
Cipate: 05-Dec-1997 #text_change 05-Dec-1997 #text_change 05-Jul-2004
Cipate: 05-Dec-1997 #text_change 05-Dec-1997 #text_
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
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A;Cross-references: UNIPROT:034977; GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB14979.
A;Experimental source: strain 168
C;Genetics:
                                                                                                                        A;Residues: I-4464 <STO>
A;Cross-references: GB:chr_I; PIDN:AAB37647.1; PID:g1703597; GSPDB:GN00019; CESP:T21E12.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: short-chain ATP-binding cassette proteins; ATP-binding cassette homology; keywords: ATP; nucleotide binding; P-loop; 121-201/Domain: ATP-binding cassette homology <ABC>; 31-201/Domain: ATP-binding cassette homology <ABC>; 38-45/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtp-binding protein typA/bipA [imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C;Accession: AB3562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABC transporter (ATP-binding protein) homolog ythP - Bacillus subtilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Pred. No. 20;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 FLOTED-SWVPAS------PDTGLDPLTVR--RHVPAVWV 35
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
24.5%; Score 54; DB 2; I
Best Local Similarity 37.8%; Pred. No. 3.7e+02;
Matches 17; Conservative 3; Mismatches 11;
                                                                                                                                                                                                                                            A,Gene: T21E12.4
A,Map position: 1
C,Superfamily: dynein heavy chain, cytosolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 FLQTEDSWVPASPDTGLDPLTVRRHV 30
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Best Local Similarity 42.3%;
Matches 11; Conservative 4
                                        Status: preliminary
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                                                                            A; Molecule type: DNA
A; Accession:
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polyketide synthase - Streptomyces hygroscopicus
C;Species: Streptomyces hygroscopicus
C;Species: Streptomyces hygroscopicus
C;Species: Streptomyces hygroscopicus
C;Accession: T30228
R;Aparicio, J.F.; Molnar, I.; Schwecke, T.; Koenig, A.; Haydock, S.F.; Khaw, L.E.; Stau Gene 169, 9-16, 1996
A;Title: Organization of the biosynthetic gene cluster for rapamycin in Streptomyces hy A;Reference number: Z20782; MUID:96186896; PMID:8635756
A;Accession: T30228
A;Accession: T30228
A;Residues preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-6260 cAPA>
A;Cross-references: UNIPROT:Q54299; EMBL:X86780; NID:g987088; PID:g987102; PIDN:CAA6046
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C;Species: Xylella fastidiosa
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: C8256
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence 406, 15-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:0910347
A;Note: for a complete list of authors see reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Circuiar carrier protein
Circuia. 3-oxoacyl-[acyl-carrier-protein] synthase I homology <0AS1>
F;55-451/Domain: 3-oxoacyl-[acyl-carrier-protein] synthase I homology <0AS1>
F;1536-1607/Domain: acyl carrier protein homology <ACP2>
F;3123-3194/Domain: acyl carrier protein homology <ACP2>
F;3123-3194/Domain: acyl carrier protein homology <ACP2>
F;3125-3999/Domain: acyl carrier-protein] synthase I homology <0AS3>
F;314-5185/Domain: acyl carrier-protein] synthase I homology <AMT1>
F;514-5185/Domain: acyl carrier protein homology <ACP3>
F;5242-5638/Domain: acyl carrier-protein] synthase I homology <AMT1>
F;5242-5638/Domain: acyl carrier-protein] synthase I homology <AMT1>
F;515-6044/Domain: acyl carrier protein homology <ACP3>
F;515-6044/Domain: acyl carrier protein homology <ACP4>
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39.3%; Pred. No. 7.2e+02;
tive 4; Mismatches 13;
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Length 301;

DB 2;

Indels

9

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A;Residues: 1-301 cHAY>
A;Cross-references: UNIPROT:P58070; GB:BA000007; PIDN:BAB36855.1; PID:g13362903; GSPDB:CA:Cross-references: UNIPROT:P58070; GB:BA100007; PIDN:BAB3685.1; PID:g13362903; GSPDB:CG:CG-GENCETCS:
C;Genetics:
A;Gene: ECB3432
C;Superfamily: ras transforming protein; translation elongation factor Tu homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable membrane protein STV2645 [imported] - Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Date: D9-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AH0807
E;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, L. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable quinate dehydrogenase [imported] - Agrobacterium tumefaciens (strain C58, Cerec C5, Species Agrobacterium tumefaciens C;bacies 22-0ct-2001 #sequence_revision 22-0ct-2001 #text_change 09-Jul-2004 C;Accession: B98314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rigoodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2333-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tun A; Reference number: A97359; MUID:21608551; PMID:11743194
A; Accession: B98314
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q8UAL9; GB:AE007870; PIDN:AAK90036.1; PID:g15160013; GSPDB:C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AL513382; PIDN:CAD07642.1; PID:g16503629; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: AGR L 2936
A;Map position: linear chromosome
C;Superfamily: glucose dehydrogenase (pyrrologuinoline-guinone)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |:|| :: :: || | :|||:|:139 LQFLASQMNFLDIVPISAETGLNVATIAAIVRKHLP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 TEDSWVP-----ASPDTGLDPLTVRRHVPAVWVLLSRDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LRFLQTEDSW---VPASPDTGLDPLT----VRRHVP 31
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37.5%; Pred. No. 42;
tive 4; Mismatches
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Pred. No. 88;
2; Mismatches
                                                                                                                                                                                                                                                                                                          Query Match
23.9%; Score 52.5; D
Best Local Similarity 38.9%; Pred. No. 30;
Matches 14; Conservative 9; Mismatches
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23.9%;
Best Local Similarity 45.2%;
Matches 14; Conservative 2
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nes 15; Conservative
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A;Molecule type: DNA
A;Residues: 1-411 <PAR>
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A; Residues: 1-809 < KUR>
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Matches
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                          Accessive termination of the control of the control
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CJP-binding protein [imported] - Escherichia coli
CiSpecies: Escherichia coli
CiSpecies: Escherichia coli
CiSpecies: Escherichia coli
CiAccession: E85902
Riperna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Alller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A.Reference number: A85480; MUD:21074935; PMID:11206551
A.Reference number: A85480; MUD:21074935; PMID:11206551
A.Residues: preliminary
A.Molecule type: DNA
A.Residues: 1-301 <STO>
A.Residues: 1-301 <STO>
A.Residues: 1-301 <STO>
A.Residues: 1-301 <STOA
A.Resperimental source: strain 0157:H7, substrain EDL933
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H91057
GTP-binding protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050995
GTP-binding protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050995
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Accession: H91057
R;Hayashi, T; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: ras transforming protein; translation elongation factor Tu homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |:|| :: :: || | :|||:|
139 LQFLASQMNFLDIVPISAETGLNVATIAAIVRKHLP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 RFLOTEDSWVPAS---PDTGLDPLTVRRHVPAVWVL 36
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Pred. No. 23;
6; Mismatches
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36.1%;
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Best Local Similarity 36.13
Matches 13; Conservative
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A;Residues: 1-236 <SIM>
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C;Genetics:
A;Gene: XF2359
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396 PGNPDITKLPPPGGTYTRSTPNVWASMSYDP 426

Search completed: January 26, 2005, 15:07:33 Job time : 9.2 secs

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Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC032136; AAH2136.1;
Genew; HGNC:19909; C9orf23.
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ProDom; PD010497; Alba DUF78; 1.
SEQUENCE 163 AA; 17631 MW; 442C8727191A0BCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               th 100.0%; Score 220; DB 2; Similarity 100.0%; Pred. No. 3.7e-21; 41; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                  Name=C9orf23;
Homo sapiens (Human).
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Best Local Similarity
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QBN5L8
QBN5L8;
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QBN5L8
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                                                              January 26, 2005, 14:40:40; Search time 43.9186 Seconds (without alignments) 537.138 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                      US-10-057-813-14_COPY_85_125
220
1 TKLRFLQTEDSWVPASPDTG......DPLTVRRHVPAVWVLLSRDP
        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                          1825181 segs, 575374646 residues
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Q8CLD8
AAS62645
Q8ZD68
Q6NNC7
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Maximum Match 100%
Listing first 45 summaries
                                             - protein search, using sw model
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AAR96155
Q82GR6
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Q72B09
AAS96307
Q8HMI6
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Q8LMV2
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09CYX4
06DGS1
091WE3
09NX88
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Gapop 10.0 , Gapext 0.5
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TISSUB-Skin;

WEDLINE=22388257; PubMed=12477932;

WEDLINE=22388257; PubMed=12477932;

Ratausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratausberg R.L., Colline F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Ratachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Lischnis B.F., Marushia K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Ugdin T.B., Toshiyuki S., Carninoi P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Robers S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley A.C., Shevchenko Y., Bouffard G.G.,

Richards S., Would A., Young A.C., Shevchenko Y., Bouffard G.G.,

Richards R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Richards S.J., Marra M.A., Shalska U., Smailus D.E., Schnerch A., Schein J.E.,

Rydones S.J., Marra M.A., Shalska U., Smailus D.E., Schnerch A., Schein J.E.,

Rydones S.J., Marra M.A., Soles M., Shalska M., Sada M., Shalska M., Shalsk
                                               Aas70926 leptospir
091013 caenorhabdi
081910 caenorhabdi
02088 caenorhabdi
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Aaq1803 symbiont
0862pl oryza sativ
09971 mus musculu
06241 mus musculu
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    Q8f6d0 leptospira
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence u
01-UN-2003 (TrEMBLrel. 24, Last annotation
Chromosome 9 open reading frame 23 protein.
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062041
BAC98031
Q8F6D0
AAS70926
Q9NDT3
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Q2088
Q8MQ20
Q8FXN6
Q8YDW0
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AAQ91803
Q8S2P1
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SEQUENCE FROM N.A.
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Akimura T., Fukunishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojina Y., Konon H., Kowda M., Koya S., Kurihara C.,
A Rawai J., Kojina Y., Konon M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Saobe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Filma Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
A Muramatsu M., Hayashizaki Y.,
L Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=C57BL/6J; TISSUE=Whole body;

MEDLINE=20530913; PubMed=11076861;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Mateuwoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Wateuwra S., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Mateuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Riki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                     01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2810432D09 product:hypothetical protein, fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musi
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CS7BL/6J; TISSUE=Whole body;
MEDLINE=9927953; PubMed=10349636;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                  163 AA.
                                                                   Created)
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STRAIN-C57BL/6J; TISSUE=Whole body;
The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Whole body;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIR=CSPBL/GJ; TISSUE=Whole body;
MEDIJNE=21085660; PubMed=11217851;
RIKEN FANTOM CONSORTIUM;
             PRELIMINARY;
                                                                                                                                                                                                                                                    Mus musculus (Mouse).
                                                                                                                                                                                            insert sequence.
Name=2810432D09Rik;
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                                                                01-JUN-2001
          Diopsy.;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MALasher R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Joedan H., Moore T., Max S.I., Wang J., Haich F.,

Mobrins R.F., Joedan H., Moore T., Max S.I., Wang J., Haich F.,

Man S.S., Loquellan M.S., Peters A.A., Rubin G.M., Hong L.,

Raha S.S., Loquellano M.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Abramson R.D., Mullahy S.J.,

Moladon D.K., Muzny D.M., Sodergren R.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Multing M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Modriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Makesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Modes S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse colly a generaces."
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TISSUE=Mammary tumor. MMTV-LTR/INT3 model. 5 month old mouse. Taken by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
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Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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Strausherg R.;
Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ293897, CAC34588.1;
EMBL; AJ293897, CAC34588.1;
EMBL; BC047068; AAH47068.1;
MGD; MGI:1917211; 2810432D09Rik.
InterPro; IPR011574; Alba DUF78.
ProDom; PD1101977; Alba_DUF78; 1.
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TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRDP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 AA; 17675 MW; 87675201AF87F5B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRDP 41
                                                                                                                                                                                      01-OCT-2004 (TrENBLrel. 17, Last sequence update)
Hypothetical protein (RIKEN cDNA 2810432D09),
Mus microllogate,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nat1. Acad. Sci. U.S.A. 99:16899-16903(2002)
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98.2%; Score 216; DB 2;
Best Local Similarity 97.6%; Pred. No. 1.3e-20;
Matches 40; Conservative 0; Mismatches 1;
                                                                                                                                   163 AA
                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-OCT-2004 (TrEMBLrel. 28,
                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Skeletal muscle;
                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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genea.";

199 AA.

PRT;

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PRELIMINARY;
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                                                                                                                                                                                    Mus musculus (Mouse)
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                                                                                                                                                                                                                                              NCBI TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Eye;
                                                                                                                                                                 Name=Rpp25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rausner R.D., Colline F.S., Wagner L., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C.,
Romnstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Frange C.,
Romnstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Frange C.,
Romnstein M.J., Worley K.C., Hale S., Garca A.M., Gay L.J., Hulyk S.M.,
N. Hichards S., Worley K.C., Hale S., Garca A.M., Gay L.J., Hulyk S.W.,
N. Halton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rachada S., Worley K.C., Sheverchenko Y., Bouffard G.G.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Nhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Nones S.J., Marra M.A.,
Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.

Brachydanio rerio (Zebrafish) (Danio rerio).

Brachydanio rerio (Zebrafish) (Danio rerio).

Brachydanio rerio (Zebrafish) (Danio Actiopata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

Cyprinidae; Danio.

NCBI_TAXID=7955;
                                                                                                                                                                                        Gaps
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                                                                                                                                        Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg R.; Strausberg R.; Submitted (UUL-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BOT05268; AAH76268.1; -. Hypothetical protein. SEQUENCE 224 AA; 24369 MW; C2FD38C9D8B2F38A CRC64;
                                                                               Hypothetical protein. —
SEQUENCE 163 AA; 17648 MW; DC89421F4F617429 CRC64;
                                                                                                                                                                                                                                                 TKGRFLQTEDSWVPTSPDTGLDPLTVRRHVPAVWVLLSRDP 125
                                                                                                                                                                                                                          1 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRDP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 TKLAYRTLQDVWEPLEPGAGLDSLTVSRNVPSIWVLLSRD 143
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                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2004 (TrEMBLrel. 28, Created)
01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                          Match 98.2%; Score 216; DB 2; Local Similarity 97.6%; Pred. No. 1.3e-20; tes 40; Conservative 0; Mismatches 1;
EMBL; AK01322; BAB28723.1; -- MGD; MG1.1917211, 2810432009Rik. InterPro; IPR011574; Alba DUF'8. ProDom; PD010497; Alba_DUF'8; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA sequences.";
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Matches
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RESULT **091WE3**

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REDLINE=22388257; PubMed=12477932;

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Altschul S.F., Collins F.S., Wagner L., Sheanen C.M., Schuler G.D.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

Bottchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Gaimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DIGATINE-20499374; PubMed=11042159; MEDLINE-20499374; PubMed=11042159; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Muramatsu M., Hayashizaki Y.; Pubtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                RIKEN full-
                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                             01-DEC-2001; (TrEMBLrel. 19, Created)
01-DEC-2001; (TrEMBLrel. 19, Last sequence update)
01-DC-2004 (TrEMBLrel. 28, Last annotation update)
Ribonuclease P 25kba subunit (Mus musculus ES cells cDNA, RIKEN length enriched library, clone:C330033C13 product:hypothetical
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                                                         protein, full insert seguence).
$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}}\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}$\dar{\}}\dar{\}$\dar{\}$\dar{\}$\dar{\}}\dar{\}$\dar{\}$\dar{\}}\dar{\}$\dar{\}$\dar{\}}\dar{\}$\dar{\}}\dar{\}$\dar{\}}\dar{\}$\dar{\}}\dar{\}$\dar{\}}\dar{\}$\dar{\}}\dar{\}}\dar{\}$\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{\}}\dar{
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TISSUENCE FROM N.A.

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TISSUESTAIN, and Skin;

MEDLINE=2238257; PubMed=12477932;

MEDLINE=238257; PubMed=12477932;

A trausher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A trausher R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A trachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Diatchenko L., Marusina F.J., Mockerna R.D., Marining P., Prange C.,

B Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Back S.A., McEwan P.-J., McKernan K.J., Malek J.M., Gaber C.P.,

R Richards S., Worley K.C., Hale S., Garcia R.D., Mullahy S.J.,

R Richards S., Worley W., Sodergren E.J., Lu X., Gibbs R.A.,

R Richards S., Worley S., Schwitz J., Lu X., Gibbs R.A.,

R Richards M.M., Touchman J.W., Green E.D., Dickson M.C.,

R Radiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

M Maring M.J., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-1998191; PubMed=12003489;
MEDLINE-1998191; PubMed=12003489;
Guerrier-Takada C., Eder P.S., Gopalan V., Altman S.;
Guerrier-Takada C., Eder P.S., Gopalan V., Altman S.;
Rutaction and characterization of Rpp25, an RNA-binding protein subunit of human ribonuclease P.";
RNA 8:290-255(2003).
RNA 8:290-255(2003).
EMBL; BC002497; AAH02497.1; -.
EMBL; AY034074; AAK54443.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                               1 TKLRFLQTEDSW--VPASPDTGLDP-----LTVRRHVPAVWVLLSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
RPP25 protein (RNase P protein subunit p25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sci. U.S.A. 99:16899-16903(2002).
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ProDom; PD010497; Alba_DUF78; 1.
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Best Local Similarity 33.3%
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IntAct; Q9BUL9; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad.
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                                                                                                                                                                                                                                                                                                                              Name=RPP25;
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                                                                                                                                                                                                                                                                                                                                                                                                                Adachi J., Alzawa K., Akimura T., Arakawa T., Bono H., Carninci P., Rykuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hanagaki T., Haraoka T., Hirozane T., Hayatsu K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki R., Maraca M., Nakamura M., Nakamura M., Saito R., Saito H., Saito H., Sakai C., Sakai K., Sakazume N., Sano H., Saito R., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Yawai C., Sakai K., Duby M., Hayashizaki T., Submitted (Apr-2002) to the BMBL/GenBank/DDBJ databases.

BMBL; AKOBSE2; BACISBG36:1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                     MEDLINE=20530913; PubMed=11076861; Shibate K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Warahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., RISHIKA integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,

Tanigami A., Fujiwara T., Ono T., Suzuki Y., Obayashi M., Nishi T.,

Hirao M., Ohmori Y., Ota T., Suzuki Y., Isogai T., Sugano S.;

Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AK000381; BAA91128.1; --

InterPro; IPR011574; Alba DUF78.

Probom; PD010497; Alba DUF78; 1.

SEGUENCE 199 AA; 20660 MW; 855494F0366B2291 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.4%; Score 69; DB 2; Length 199; llarity 33.3%; Pred. No. 0.64; Conservative 11; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
30.9%; Score 68; DB 2; Length 199;
Best Local Similarity 33.3%; Pred. No. 0.87;
Matches 16; Conservative 10; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TKLRFLQTEDSW--VPASPDTGLDP-----LTVRRHVPAVWVLLSRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nl protein.
199 AA; 21037 MW; B9DE105BE3293D64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OM-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ20374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:2143151; AI851155.
InterPro; IPR011574; Alba_DUF78.
ProDom; PD010497; Alba_DUF78; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 16; Conserv
             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J;
                                     STRAIN=C57BL/6J;
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Q9NX88; **09NX88**

RESULT 6

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Gaps
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                                                     DB 2; Length 199;
                                                                                                                          TKLRFLQTEDSW--VPASPDTGLDP-----LTVRRHVPAVWVLLSRD
                                                                                                                                           14; Indels
PD010497; Alba DUF78; 1.
3 199 AA; 20632 MW; 9A4494F0297B2A81 CRC64;
                                                   30.9%; Score 68; DB 2;
33.3%; Pred. No. 0.87;
tive 10; Mismatches
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3

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(Rel. 41, Created)
                                                       Name=ZNF324:
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SEQUENCE
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Matches
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                                                                                                                                                                                                                      TISSUE=Uterus;

WEDLINE=22388257; PubMed=12477932;

WEDLINE=22388257; PubMed=12477932;

WEDLINE=22388257; PubMed=12477932;

WA Stausberg R.L., Fealigold E.A., Grouse L.H., Derge J.G.,

Rausner R.D. Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Altechul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

HOPKINS R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Atapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Ry Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

RA Gones S.J., Marra M.A.;

RA "Generation and initial annalysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC007717; AAH07717.1; -.
G0; G0:000534; C:nucleus; IEA.
G0; G0:0008270; F:nucleic acid binding; IEA.
G0; G0:0008270; F:zinc ion binding; IEA.
G0; G0:000835; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR001099; KRAB.
InterPro; IPR001005; Myb DNA binding.
InterPro; IPR007087; Znf_C2HZ.
                                                                                                                                              Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
 95 TRLRYRSVREVWQSLPPGPTQGQTPGEPAASLSVLKNVPGLAILLSKD 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50805, KRAB; 1.
PROSITE; PS00037, MYB 1; UNKNOWN 1.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 1.
SEQUENCE 286 AA; 31762 MW; IFC850BC630DC71B CRC64;
                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30.5%; Score 67; DB 2; 46.4%; Pred. No. 1.8;
                                                               PRT; 286 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           553 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 EDSWVPASPDTGLDPLTVRRHVPAVWVL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 EEPWVPSGTDTTLSRTTYRRRNPGSWSL 84
                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam, PF01352, KRAB, 1. SMART, SM00349, KRAB, 1. SMART, SMO0355, ZnF C2H2, 1.
                                                                                        01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 46.4%;
Conservative
                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=Uterus;
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                  ZNF324 protein.
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ID Z324_HUMAN
AC 075467;
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                                                                 096198
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Kim B.W., Cho H.M., Jun D.Y., Kim Y.H.;

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: May function as a transcription factor.

-I- SUBCELLULAR LOCATION: Nuclear (Probable).

-I- SIMILARITY: Belongs to the krueppel C2H2-type zinc-finger protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001909; KRAB.
InterPro; IPR001909; KRAB.
InterPro; IPR001909; KRAB.
InterPro; IPR001909; KRAB.
InterPro; IPR001905; KRAB; I.
Pfam; PP00066; zf-C2H2; 9.
ProDom; PD000003; Znf_C2H2; 9.
SMART; SM00349; KRAB; I.
SMART; SM00349; KRAB; I.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 9.
PROSITE; PS00028; ZINC_FINGER_C2H2_2; 9.
DNA-binding; Metal-binding; Nuclear protein; Repeat;
Transcription regulation; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C2H2-type 9.
BBCB5C469A13108F CRC64;
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Zinc finger protein 324 (Zinc finger protein ZF5128)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2013 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 28, Last annotation update)
Hypothetical (Putative membrane protein).
Name=icmF2; OrderedLocusNames=YP2442, y1553;
                                                                                                                                                                                                                                                                                                                                                                                                   family.
--- SIMILARITY: Contains 9 C2H2-type zinc fingers.
--- SIMILARITY: Contains 1 KRAB domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 1192 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C2H2-type 1.
C2H2-type 2.
C2H2-type 3.
C2H2-type 4.
C2H2-type 5.
C2H2-type 5.
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C2H2-type 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF060503; AAC33716.1; -. HSSP; P08047; 1SP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61104 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 46.4%;
nes 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genew; HGNC:14096; ZNF324.
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                                                                                                       Homo sapiens (Human)
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285
313
341
341
423
423
453
53 AA;
                                                                                                                                                                           NCBI_TaxID=9606;
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Q8CLD8; Q74SW5;
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Yersinia pestis.

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MEDLINE-20-92 / Biovar Orientalis;
MEDLINE-21470413; PubMed=11586360; DOI=10.1038/35097083;
MEDLINE-21470413; PubMed=11586360; DOI=10.1038/35097083;
Parkhill J., Waren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Genome sequence of Fyerinia pestis, the causative agent of plague.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Berkeley;
Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
Burk S., Wan K., Yu C., Rubin G.M., Celniker S.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BT011363; AAR96155.1;
SEQUENCE 206 AA; 23162 MW; 8B9FD01C279BC5D9 CRC64;
                                                                                                                                                                                                                 Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ebhydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 206;
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29.1%; Score 64; DB 2; Length 206
Best Local Similarity 30.0%; Pred. No. 3.1;
Matches 12; Conservative 10; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRD 40
                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.2%; Score 66.5; DF 47.1%; Pred. No. 11; tive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    206 AA
                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; AD0332; AD0332.
InterPro; IPR010623; DUF1215.
InterPro; IPR009612; ImcF-related.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF06744; DUF1215; 1.
Pfam; PF06761; ImcF-related; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 413:523-527(2001).
EMBL; AJ414153; CAC92963.1; -.
                                                                                                 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2004 (TrEMBLrel. 26, Putative membrane protein. OrderedLocusNames=YPO2724;
                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Best Local Similarity
Matches 16; Conserv
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                                                                                                                                                                                                 Yersinia pestis
                                                                                                                                                                                                                                                        NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=CG9422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6NNC7;
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                           RESULT 12
Q8ZD68
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                                                                                      SEQUENCE FROM N.A.
STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=221378663; PubMed=12142430;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                Zhou D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=91001 / Biovar Mediaevalis;
Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
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                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=91001 / Biovar Mediaevalis;
SONG Y., TONG Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z., Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P., Yang R.;
                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 1192 AA; 135060 MW; C53ECD6EAlD8804F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases. EMBL; AE013758; AAM85122.1; -. EMBL; AE017136; AAS62645.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yang R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
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24-MAR-2004 (TrEMBLrel. 27, Last sequence update)
24-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Putative membrane protein.
ICMF2 OR YP2442.
Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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6; Mismatches
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                                                                                                                                                                                                                                            "Genome sequence of Yersinia pestis KIM.";
J. Bacteriol. 184:4601-4611(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.2%; Score 66.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR010623; DUF1215.
InterPro; IPR009612; ImcF-related.
Pfam; PF06744; DUF1215; 1.
Pfam; PF06761; ImcF-related; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.18;
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es 16; Conservative
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                                                        NCBI_TaxID=632;
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AAS62645;
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Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Fribe B., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
MEDLINE=22426069; PubMed=12537572;
Mille B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                   "Annotation of the Drosophila melanogaster euchromatic genome:
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Match 29.1%; Score 64; DB 2; Length 206; Local Similarity 30.0%; Pred. No. 3.1; les 12; Conservative 10; Mismatches 16; Indels
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Stapleton M., Carlson J., Chavez C., Frise E., George R.,
Stapleton M., Yu C., Rubin G.M., Celniker S.;
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BT011363; AAR96155.1;
SEQUENCE 206 AA; 23162 MW; 8B9FD01C279BC5D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16; Indels
                                                                                                                                                                                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases EMBL, AE003790; AAM70814.1; -. IntAct, Q9V9B6; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FlyBase, FPgn0033092, CG9422.
SEQUENCE 206 AA; 23146 MW; 9FCFDF4C3C9BC5D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRD 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                  a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
                                                                                                                                                                                                                                                                                                                     Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
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MEDLINE=22426070; PubMed=12537573;
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AAR96155;
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1 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRD 40

Search completed: January 26, 2005, 15:06:29 Job time : 45.9186 secs

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220
1 TKLRFLQTEDSWVFASPDTG......DPLTVRRHVPAVWVLLSRDP 41
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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1: geneseqp1980s:*
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aag89339 Human sec	Abu00014 Human nov	Adm90988 Human pha	Aay36104 Extended		_	Adq17615 Human sof	ທ	Abb64410 Drosophil	Abp05282 Human_ORF	Abo64395 Klebsiell	Adj71002 Human hea	Adc36134 Weed cont	Adol3847 Protein e	9	Aar43576 Bovine ad	Aag51877 Arabidops	_	Aag51848 Arabidops	•		æ	Aag51875 Arabidops	_	~
ID	AAG89339	ABU00014	ADM90988	AAY36104	ADP19412	AAM38973	ADQ17615	ADN99926	ABB64410	ABP05282	AB064395	ADJ71002	ADC36134	ADO13847	ABG21326	AAR43576	AAG51877	AAG16840	AAG51848	AAG16839	AAG51876	AAG16838	AAG51875	AAG51847	ADN72883
DB	4	ø	α	N	ω	4	ω	œ	4	S	7	7	7	œ	4	~	m	ო	ო	m	ო	m	m	m	æ
% Query Match Length	163	163	219	163	163	211	553	558	205	96	586	1037	408	4083	264	266	298	298	314	314	314	350	350	350	350
% Query Match	100.0	100.0	100.0	88.2	88.2	30.9	30.5	30.5	29.1	28.0.	28.0	26.4	25.9	25.7	25.5	25.5	25.5	ς.	ű.		S.	25.5	S.	ď.	25.5
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Adn72183 Thale cre Aag51846 Arabidops Abu2856 Human pro Aam7855 Human pro Aam78539 Human NOV Abj39112 Molecule Adc03509 Deinococc Aau53860 Propionib Abm50399 Propionib Abm50399 Propionib Abu44710 Protein e Adb70297 C. neofor Abo55560 Human gen Aby37461 S. Kaniha Abu32194 Protein e Abo63127 Klebbiell Aab23464 Wheat LLS Aam40741 Human pol Aag33137 Zea mays			vaccine; treatment; diagnosis;	C	Jobert S; encoding potentially secreted accination against a variety of leeases.	ET human nucleic acids encoding c acids and the polypeptides t. treatment and diagnosis of NSET gene expression. For associated with decreased GENSET or by supplementing the cides. Conversely, antisensed to down regulate GENSET genes and preventing their genes and preventing their ic acids may also be used as DNA ic acids may also be used as DNA
B ADD72183 3 AAGS1046 4 AAW76555 4 AAW76555 4 AAW76555 6 ABU33112 7 ADC03509 6 ABW4710 7 ABU4710 7 ABU70297 6 ABW31139 3 AAB23464 4 AAW40741 3 AAG33137	ALIGNMENTS protein; 163 AA.	ry) SEO ID NO: 459	gene therapy;	938. 29P. 70P.	acugueleret L, nucleic acids therapy and ve sis of those di	ull length GENS. The nuclei, the prevention reat disorders, ing mutations o ivity of GENSET GENSET polypep be administere the cells' own antisense nucle
56 25.5 350 9 55.5 25.5 350 9 55.5 25.2 1370 1 55.5 25.2 1370 2 55.5 25.2 1370 3 55.5 25.2 1397 2 55.5 25.2 1446 3 55.5 25.2 1446 4 54.5 24.8 98 54 24.8 98 54 24.8 1124 6 54 24.5 1246 1 53 5 24.8 1124 8 54 24.5 1246 1 53 5 24.5 1246 1 53 5 24.5 1246 2 53 24.1 185 5 5 5 2 5 2 148 1 5 5 5 2 5 2 148 2 6 7 7 8 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1 39 \G89339 standard;	AAG89339; 11-SEP-2001 (first entry) Human serreted protein. GE	secreted pro T. Bapiens.	M-2001. 2-2000; 2000WO- 2-1999; 99US- R-2000; 2000US-) GENSET.	Numas Milne Edwards J, 1871, 2001-367870/38. N-PSDB; AAH64942. Full length GENSET human proteins, useful in gene diseases, and for diagnos Claim 21; Page 910-911;	The invention relates to forth potentially secreted prote they encode may be used in diseases associated with it example, they be used to t gene expression by rectify ganome that affect the act patients own production of nucleic acid molecules may expression by binding with expression. The sense and
ଭିତାରିଭିଲିଲେଲିଲିଲିଲିଲିଲିଲିଲେକସଂସଂସଂସଂସ	SUL 389					\$88888888888

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29-AUG-
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probes in diagnostic assays to detect and quantitate the presence of similar nucleic acid sequences in samples, and hence to determine which patients may be in need of restorative therapy. The GENSET polypeptides may be used as antigens in the production of antibodies and in assays to identify modulators (agonists and antaqonists) of GENSET polypeptide expression and activity. The present sequence is a GENSET polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polypeptides and polynucleotides, useful for preventing, treating or ameliorating medical conditions, such as cancer, neurodegenerative disorders, lymphoid cell disorders, bone degenerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human, genetic disorder, gene mapping, medical imaging, cancer, neurodegenerative disorder; lymphoid cell disorder; osteoporosis; Parkinson's disease, Alzheimer's disease, bone degenerative disorder; osteoarthritis; periodontal disease; liver fibrosis; viral infection; fungal infection; autoimmune disease; diabetes;
                                                                                                                                                                                                                Gaps
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R, Wang Z, Ghosh M;
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0
                                                                                                                                                                              Length 163;
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                41
                                                                                                                                                                                                                                            1 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRDP
                                                                                                                                                                          Score 220; DB 4;
Pred. No. 8.2e-23;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rang YT, Zhou P, Goodrich R, Asundi V,
Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen
Wehrman T, Wang J, Wang D, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 9; SEQ ID NO 633; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                ABU00014 standard; protein; 163 AA
                                                                                                                                                                                                            .,
                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human novel polypeptide #107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disorders, and infections.
                                                                                                                                                                                                              Conservative
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N-PSDB; ABX05092.
                                                                                                                                                                                          Local Similarity
hes 41; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atopic dermatitis.
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                                                                                                                                          Sequence 163 AA;
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                                                                                                                                                                          Query Match
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Matches
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nootropic;
Sequences ABG99888-ABG99989 and ABU00010-ABU00433 represent human polypeptides of the invention. Note: The sequence data for this patent not represented in the printed specification but is based on sequence
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              cardiovascular disorder; ischaemic heart disease; acute myocardial infarction; respiratory disease; acute myocardial disorder; peptic ulcer; cirrhosis; immune disorder; HIV infection; systemic lupus erythematosus; endocrine system; diabetes mellitus; epilepsy; Alzheimer's disease; amujotropic lateral sclerosis; skin disorder; psoriasis; bacterial; thrombolytic; antianaemic; cardiant; vasotropic; antiasthmatic; antianaemic; cardiant; vasotropic; antiasthmatic; antiantentic; antidiabetic; dermatological; antirheumatic; antianaemic; antianaemic; antipacterial; fungal; perceive; nootropactic; antibacterial; fungicide; antiparasitic; virucidal;
                                                                                                                                              ö
                                                                                                                Length 163;
                                                                                                                                            Indels
                                                                                                                                                                                                          85 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRDP 125
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                                                                                                                                                                                                                                                                                                                                                                                                                    human; cancer; haematopoiesis; thrombosis; anaemia;
                                                                                                                                                                            1 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRDP
                                              information supplied by the European Patent Office
                                                                                                             100.0%; Score 220; DB 6;
100.0%; Pred. No. B.2e-23;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                   Human pharmaceutically useful protein SegID 381.
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                                                                                                                                                                                                                                                                                        ADM90988 standard; protein; 219 AA
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2002US-0406666P.
2002US-0410946P.
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2002US-0406612P.
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2002US-0406640P.
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2002US-0410953P.
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                                                                                              Query Match
Best Local Similarity 100..
                                                                                                                                                                                                                                                                                                                                                     03-JUN-2004 (first entry)
                                                                               Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004020595-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy;
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29-AUG-2002;
17-SEP-2002;
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17-SEP-2002;
17-SEP-2002;
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This sequence is encoded by an extended human secreted protein coding sequence of the invention. The secreted proteins can be used in treating or controlling a variety of human conditions. The secreted proteins may act as cytokines or may affect cellular proliferation or differentiation or may act as immune system regulators, haematopolesis regulators, tissue growth regulators, regulators of reproductive hormones or cell movement or have chemotactic/chemokinetic, receptor/ligand, anti-inflammatory or tumour inhibition activity. The DNAs can be used in forensic procedures to identify individuals or in diagnostic procedures to identify individuals or in diagnostic procedures to individuals having genetic diseases resulting from abnormal expression of the genes corresponding to the extended cDNAs. They are also useful for constructing a high resolution map of the human chromosomes. They can also be used for gene therapy to control or treat genetic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dumas Milne Edwards J, Bougueleret L, Jobert S, Clusel C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88.2%; Score 194; DB 2; Length 163; 87.8%; Pred. No. 3.9e-19; ive 0; Mismatches 5; Indels
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                                                                                                                                                                                                                                Dumas Milne Edwards J;
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                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 423-424; 516pp; English.
                                                                                                                                                                                                                                                                                                                              New isolated human secreted proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADP19412 standard; protein; 163 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human secreted polypeptide #263.
                                                                                   97US-0069957P.
98US-0074121P.
98US-0081563P.
98US-0096116P.
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21-JUN-2000; 2000WO-IB000951
15-SEP-2000; 2000US-00663600
                                              98WO-IB002122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-2001; 2001US-00978360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-1998; 98WO-IB002122
                                                                                                                                                                                                                                Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 87.8 ies 36; Conservative
                                                                                                                                                                                                                                                                   WPI; 1999-385906/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEST ) GENSET SA.
                                                                                                                                                                                                                                                                                        N-PSDB; AAX97788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 163 AA;
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                                                                                                                                                                                                                             Bougueleret L,
                                                                                                                                                                                  (GEST ) GENSET
                                                                                   17-DEC-1997;
09-FEB-1998;
13-APR-1998;
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                                              17-DEC-1998;
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                                                                                                                                              10-AUG-1998;
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      24-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
                                                                                                                                                                                                                                                                                            This invention relates to novel isolated human polynucleotides and the encoded proteins thereof. Specifically, it refers to proteases, kinases, phosphatases, secreted and transmembrane proteins, as well as the derived composition of the present invention describes polypeptides.

Comparison the present invention describes polypeptides, preventing and treating proliferative disorders, e.g. cancer, disorders of and treating proliferative disorders, e.g. cancer, disorders of nameropoiesis such as thrombosis and anaemia, cardiovascular disorders, e.g. ischaemic heart disease and acute myocardial infarction, respiratory diseases, e.g. asthma, pneumonia or cystic fibrosis, disorders of kidney and urinary tract, e.g. chronic renal failure and glomerulopathy, gastrointestinal disorders, e.g. peptic ulcer or cirrhosis, immune disorders, e.g. peptic ulcer or cirrhosis, immune disorders, e.g. epilepsy, Alzheimer's disease or amyotropic lateral coffisorders, e.g. epilepsy, Alzheimer's disease or amyotropic anterious coffisorders, e.g. epilepsy, Alzheimer's disease or amyotropic anterious cofficiant varial diseases. Accordingly, they exhibit many various cofficiance and viral diseases. Accordingly, they exhibit many various antialaemic, cardiant, vasorropic, antialesmic, antialery, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                             New human polynucleotides and polypeptides, useful for diagnosing, preventing and treating proliferative disorders, immune disorders, cardiovascular disorders, or bacterial, fungal, parasitic and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccines. This polypeptide is a human protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extended human secreted protein sequence, SEQ ID NO. 489.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRDP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 220; DB 8; 100.0%; Pred. No. 1.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                              Hestir K;
(RIKE-) RIKEN INST PHYSICAL & CHEM RES (DNAF-) DNAFORM KK.
                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 381; 254pp; English.
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                                                              Lee B,
                                                                                                                         N-PSDB; ADM90779, ADM91197
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                                                              Chu K,
                                                                                                  2004-257410/24
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Best Local Similarity
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                                                            Williams LT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 4
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(HYSE-) HYSEQ INC.

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The invention relates to human cDNA sequences that encode human secreted proteins. The invention also relates to an antibody that specifically binds to a polypeptide of the invention and a method of binding the polypeptide to an antibody. The polymucleotides are useful for expressing the entire secreted proteins which they encode and for distinguishing the calls from non-human tissues and cells, and for distinguishing between human tissues and cells, and for the polymucleotides comprising the cDNAs. The polymucleotides and the polymucleotides are useful in forensic procedures or disgnostic procedures to identify individuals with genes corresponding to the cDNAs. The sequences are also useful in gene therapy to control or treat genetic diseases. This equence represents a human secreted polypeptide of the invention. Note: The sequence data for this patent did not form part of the printed control of the printed control of the printed control of the month of the printed control of the printed control of the control of the control of the control of the printed control of the control of t
                                                                                                                     New isolated polynucleotide encoding secreted polypeptide, useful for gene therapy, or in diagnostic procedures to identify individuals having genetic diseases resulting from abnormal expression of the genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Humenostatic; amyotrophic lateral sclerols; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRDP 41
                                                                                                                                                                                                                        Claim 2; SEQ ID NO 668; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAM38973 standard; protein; 211 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88.2%; Scurer 87.8%; Pred 0; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 2118.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     segdata.uspto.gov/seguence.html
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2000US-00620312.
2000US-00653450
2000US-00662191.
2000US-00693036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-00488725
2000US-00552317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-OCT-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Conservative
                                              WPI; 2004-440404/41.
N-PSDB; ADP19007.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 163 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200153312-A1.
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19-JUL-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JAN-2000;
25-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-OCT-2000;
Duclert A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAM38973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
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Score 194; DB 8; Length 163; Pred. No. 3.9e-19; 0; Mismatches 5; Indels

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encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polymucleotides are useful in gene therapy. A composition containing a polypeptide or polymucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous localised neuropathies and central nervous system diseases, such as latelaner's, Parkinson's disease, Huntington's diseases, amyotrophic attains solerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotectic/chemokinetic activity, haemostatic and thrombolytic activity, chemotectic/chemokinetic activity, haemostatic and thrombolytic activity, arthritis and inflammation, leukaemias and c.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
                                                 Wang D;
, Zhao QA;
                                                                                                                                                 Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.
                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                               Ren F, Wa
Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 211; 0.37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TKLRFLQTEDSW--VPASPDTGLDP----LTVRRHVPAVWVLLSRD
                                               Qian XB,
Yang Y,
                                         Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Goodrich R, Drmanac RT;
                                                                                                                                                                                            Example 4; SEQ ID NO 2118; 10078pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.9%; Score 68; DB 33.3%; Pred. No. 0.37 tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zlotnik A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ17615 standard; protein; 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PROT-) PROTEIN DESIGN LABS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-NOV-2002; 2002US-0429739P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 33.39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ginsburg WM,
                                                                                                      WPI; 2001-442253/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-441208/41.
                                                                                                                    N-PSDB; AAI58129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 211 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-JUN-2004.
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Best Local Si
Matches 16;
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                                            Tang
Wang
Zhou
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15-JUL-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                       08-AUG-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams LT,
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                                   The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual data and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the expression in the first soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcome. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated protein of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                                                     anti-inflammatory; dermatological; neuroprotective; immunomodulator; antibacterial; vitucide; antipacoriatic; cytostatic; gene therapy; vaccine; inflammatory; CNS; immune disorder; cancer; psoriasis; diabetes; early aging; hormonal imbalance; ischemic heart disease;
                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                       30.5%; Score 67; DB 8; Length 553; 46.4%; Pred. No. 1.7;
                                                                                                                                                                                                                            13; Indels
                                                                                                                                                                                                                           2; Mismatches
                   Example 2; SEQ ID NO 432; 210pp; English.
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                                                                                                                                                                                                                                                           ADN99926 standard; protein; 558 AA
                                                                                                                                                                                                                                                                                                                                                                                  Novel human protein sequence #742.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2002US-0421061P
2002US-0421080P
2002US-042152P
2002US-0421517P
2002US-0422177P
2002US-0422178P
2002US-042834P
2002US-0426384P
2002US-0426384P
2002US-0426394P
2002US-0426394P
2002US-0426394P
2002US-0426394P
2002US-0426394P
2002US-0429275P
2002US-0429324P
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2002US-0430645P.
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2002US-0430657P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2002US-0430657P
                                                                                                                                                                                                                                                                                                                                                              29-JUL-2004 (first entry)
                                                                                                                                                                                                                Local Similarity 46.4
                                                                                                                                                                                                                                                                                                                                                                                                                                               ulcerative colitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004038003-A2.
                                                                                                                                                                                    Sequence 553 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-OCT-2002;
15-NOV-2002;
15-NOV-2002;
15-NOV-2002;
15-NOV-2002;
15-NOV-2002;
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04-DEC-2002;
04-DEC-2002;
04-DEC-2002;
04-DEC-2002;
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27-NOV-2002;
27-NOV-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-NOV-2002;
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                                                                                                                                                                                                                                                                                                                                          ADN99926;
                                                                                                                                                                                                        Query Match
 вагсоща
                                                                                                                                                                                                                           Matches
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The invention relates to a nucleic acid molecule comprising a polynucleotide sequence or its complement that encodes a polypeptide. The nucleic acid is useful in preparing a composition for treating or preventing inflammatory, CNS, immune, bacterial or viral disorder, cancer, psoriasis, diabetes, early aging, hormonal imbalance, ischemic theat disease or ulcerative colitis. This sequence corresponds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Beaurang PA, Behrens D;
nemann T, Pierce K, Wang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New nucleic acid molecules, useful in preparing a composition for treating or preventing e.g. inflammatory, CNS, bacterial or viral disorders, cancer, psoriasis, diabetes, ischemic heart disease or ulcerative colitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Hestir K, Beaurang
Lin H, Linnemann T,
Zeng C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 14; SEQ ID NO 1526; 532pp; English.
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04-DEC-2002; 2002US-0430668P.
05-DEC-2002; 2002US-0430684P.
05-DEC-2002; 2002US-0430684P.
05-DEC-2002; 2002US-0430684P.
12-DEC-2002; 2002US-0431458P.
12-DEC-2002; 2002US-0431458P.
12-DEC-2002; 2002US-04313251P.
13-DEC-2002; 2002US-0433316P.
13-DEC-2002; 2002US-0433316P.
13-DEC-2002; 2002US-0433316P.
13-DEC-2002; 2002US-0433316P.
13-DEC-2002; 2002US-0433316P.
17-JAN-2003; 2003US-0440821P.
18-APR-2003; 2003US-0440821P.
18-APR-2003; 2003US-0463708P.
18-APR-2003; 2003US-0463708P.
19-AAY-2003; 2003US-0467129P.
02-MAY-2003; 2003US-0467203P.
02-MAY-2003; 2003US-047330P.
19-MAY-2003; 2003US-047330P.
19-MAY-2003; 2003US-047330P.
22-MAY-2003; 2003US-0476631P.
09-JUN-2003; 2003US-0476631P.
09-JUN-2003; 2003US-0476631P.
09-JUN-2003; 2003US-0476631P.
09-JUN-2003; 2003US-0476631P.
08-JUL-2003; 2003US-0485211P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JUL-2003; 2003US-0485224P
08-JUL-2003; 2003US-0485325P
08-JUL-2003; 2003US-0485359P
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2003US-0486960P
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Halenbeck RF, Kothakota s,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein of the invention.
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Kothakota
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 46.4
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-365511/34.
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The present invention describes substantially purified human proteins

(referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
in the specification. ARNISTS to ARNIZ252 encode the human ORFX
in the specification. ARNISTS to ARNIZ252 encode the human ORFX

criminal minans, and in the manufacture of a medicament for treating a
disorder in humans, and in the manufacture of a medicament for treating a
syndrome associated with ORFX-associated disorder. ORFX polymucleotide
sequences can be used in gene therapy. ORFX sequences can be used in the
treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
psoriasis, benign tumours, keloid, degenerative disorders related to organ
transplantation, cardiovascular diseases, disorders related to organ
transplantation, cardiovascular diseases, disorders, infectious
storage disease, various immune deficiencies and disorders, infectious
diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
atthritis, autoimmune thyroiditis, myasthonia quavis, graft-versus-host
disease and autoimmune inflammatory eye disease. ORFX proteins are also
to settlusion injury in various tissues and conditions resulting from
protection or regeneration and treatment of lung or liver fibrosis,
bone degenerative disorders, or periodontal disease, and for gut
protection or regeneration and treatment of lung or liver fibrosis,
creperfusion injury in various tissues and conditions resulting from
systemic cytokine damage. N.B. The sequence data for this patent did not
form part of the printed specification, but was obtained in electronic
format directly from WIPO at fib.wipo.int/published_pct_gequences
                                                    hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; infimune deficiency; immune disorder; infectious disease; autoimmune disorder; infectious disease; myasthenia gravis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ::|||::
SRLRFVEQIRSVSPGDSTTPSLGEVYTADSWTGQPLTPLMPGSAADELS---HLPATWIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---TEDSW-----VPASPDTGLDPLTVRRHVPAVWVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human polypeptides and polymucleotides useful for diagnosing preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                    Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 5; Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 10546; 1037pp; English.
Human ORFX protein sequence SEQ ID NO:10546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.2;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 61.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000; 2000US-0206132P. 29-AUG-2000; 2000US-0228716P.
                                                                                                                                                                                                                                                                                                                29-MAY-2001; 2001WO-US010836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.0%;
26.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-106308/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ABN21034.
                                                                                                                                                                                                                                         WO200192523-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Shimkets RA,
                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                           06-DEC-2001.
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ABO64395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA BBR2072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 20022; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.1%; Score 64; DB 4; Length 205; 30.0%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRD 40
                                                                                                                                                                                                                                                    Drosophila melanogaster polypeptide SEQ ID NO 20022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.3;
10; Mismatches
         EDSWVPASPDIGLDPLIVRRHVPAVWVL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myers EW;
                                          62 EEPWVPSGTDTTLSRTTYRRRNPGSWSL
                                                                                                                                      ABB64410 standard; protein; 205 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP05282 standard; protein; 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                              26-MAR-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
Les 12, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ABL08513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 205 AA;
                                                                                                                                                                                                                                                                                                                                                                                 WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interactions
                                                                                                                                                                                                                                                                                                                                                                                                                    27-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter JC,
         σ
                                                                                                                                                                           ABB64410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP05282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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Matches
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                                                                                                  RESULT 9
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diagnosing,

36 92

Gapa

27;

Indels

9

Glenn GM;

Taylor SW,

Gibson BW,

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This invention relates to novel mitochondrial targets that can be used for therapeutic intervention in treating a disease associated with alterated mitochondrial function. Specifically, it refers to a method for identifying proteins of the human heart mitochondrial proteome that are useful for drug screening assays, as well as therapeutic targets. The present invention describes a method for identifying such proteins that can be used in the treatment of various diseases associated with altered mitochondrial function including diabetes mellitus, Huntington's disease, osteoarthritis, Leber's heredicary optic neuropathy (LHON), mitochondrial concephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy ragged red fibre syndrome (MERRP) or cancer. Accordingly, these compositions have neuroprotective, nootropic, antidiabetic, anticonvulsant, antiarthritic, osteopathic, ophthalmological and cytostatic activities. This polypeptide sequence is a human heart mitochondrial protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   weed controller metabolism; weed; herbicide; herbicide-resistant plant;
                                                                                                                                                                                                                                                                    Identifying a mitochondrial target for drug screening assays and for treating diseases associated with altered mitochondrial function, comprises detecting a modified polypeptide in a sample and correlating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 WVPASPDTGLDPLT------VRRHVPAVWVLLSRDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Weed controller metabolism protein SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 2808; 180pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC36134 standard; protein; 408 AA.
                                                                                                                                                                                           Zhang B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces phaeochromogenes.
                                                04-APR-2003; 2003WO-US010870.
                                                                                12-APR-2002; 2002US-0372843P.
17-JUN-2002; 2002US-0389987P.
20-SEP-2002; 2002US-0412418P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-OCT-2001; 2001JP-00321307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Beet Local Similarity 29.3v,
"-hea 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                            (MITO-) MITOKOR.
(BUCK-) BUCK INST AGE
                                                                                                                                                                                           Fahy ED,
                                                                                                                                                                                                                                         WPI; 2003-845369/78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1037 AA;
                                                                                                                                                                                                                                                                                                                  with the disease.
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                                                                                                                                                                                        Ghosh SS, F
Warnock DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agrochemical
                     23-OCT-2003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADC36134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae polypeptide of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                             useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mitochondrial; human; screening assay; diabetes mellitus;
Huntington's disease; osteoarthritis;
Leber's hereditary optic neuropathy; LHON;
mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
myoclonic epilepy ragged red fibre syndrome; MERRF; cancer;
neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
osteopathic; ophthalmological; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human heat mitochondrial protein as a therapeutic target SeqID2808.
                                                                                                                         Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding a Klebsiella pneumoniae polypeptide, preparing a vaccine composition against Klebsiella pneumoniae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7; Length 586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LRFLQTEDSWVPAS-PDTGL-DP-LTVRRHVPAVWVLLSRDP
                                                                                          Klebsiella pneumoniae polypeptide seqid 10912.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ID NO 10912; 932pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28.0%; Score 61.5; DF llarity 35.7%; Pred. No. 11; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADJ71002 standard; protein; 1037 AA
ABO64395 standard; protein; 586 AA
                                                                                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                   27-JAN-2000; 2000US-00489039
                                                                                                                                                                                                                                                                                                 99US-0117747P
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                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                            Osborne M;
                                                                                                                                                                     Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-895346/82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ACH97946.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 586 AA;
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                                                                                                                                                                                                                                                                                                29-JAN-1999;
                                                             29-JUL-2004
                                                                                                                                                                                                     US6610836-B1
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                                                                                                                                                                                                                                    26-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                             Breton GL,
                              ABO64395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADJ71002;
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Gapa

14;

41

13; Indels

DB 7; Length 1037;

Score 58; DB 'Pred. No. 67; 4; Mismatches

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ATCC39727 (formerly Actinomadura sp. ATCC39727). The 37 proteins encoded by the gene cluster are involved in the biosynthesis of the glycopeptide A40926. dbv ORF 1, 2, and 37 encode polypeptides required for the synthesis of 4-hydroxy-phenylglycine residues of A40926. dbv ORF 30-34 and 37 encode polypeptides required for the synthesis of 3, 5-dihydroxy-phenylglycine residues of A40926. dbv ORF 16, 17, 25, 26 and 36 encode polypeptides required for the synthesis of heptapeptide skeleton of A40926. dbv ORF 10 encodes polypeptide required for the beta-hydroxylation of the trycosine residues of amino acide required for the beta-hydroxylation of the trycosine residue of amino acide of the aromatic residues of amino acide a required for the beta-hydroxylation of the trycosine residue of amino acide of the aromatic residues of amino acide at positions 2 and 4, and 6, 1 and 3, and 5 and 7 of A40926. dbv ORF 9, 23 and 29 encode polypeptides required for the attachment of mannosyl residues or amino acide polypeptides required for the attachment of mannosyl residues or N-methylation of A40926. dbv ORF 9, 18, 19, 24 and 35 encode polypeptides required for the attachment of mannosyl residues or N-methylation of A40926 dbv ORF 7, 18, 19, 24 and 35 encode polypeptides required for the attachment of mannosyl residues or N-methylation of A40926 dbv ORF 7, 18, 19, 24 and 32 encode polypeptides required for regulating the expression of one or more genes of the dbv gene cluster. The dbv gene cluster and the proteins encoded by it are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 4083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    producing glycopeptide antibiotic A40926 or its precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2385 AYVTABEGSGLDPDAVREHLAGRLPEFMVPAAVVLLDGVP 2424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 SWVPASPDIGLDPLIVRRH-----VPAVWVLLSRDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 56.5; DB 8;
Pred. No. 5.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25.7%; Scc. 40.0%; Pred. No. 5...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel human diagnostic protein #21317.
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23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 40.0 es 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAS85513.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4083 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200175067-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          biodiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel DNA encoding a weed controller metabolism protein. A protein of the invention has herbicide activity. The proteins and their encoded genes are useful e.g. in constructing new breeds of herbicide-resistant plants and also in developing various agrochemicals. The present sequence is used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dbv; gene cluster; Actinomadura sp.; biosynthesis; glycopeptide; A40926; 4-bydxoxy-phenylglycine; 3; 5-dhydxoxy-phenylglycine; heptapeptide skelecon; chlorination; aromatic residue; beta-hydroxylation; tyrosine; cross-linking; N-acetyl glucuroamine;
                                                                                                                                                                                                            Weed controller metabolism proteins deactivating porphyrinogen oxidase (PPO)-inhibiting herbicides by N-demethylation and their genes, useful e.g. in constructing new breeds of herbicide-resistant plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 EDSWVPASPDTGLDPLTVRRHVP-----AVWVLLSRD 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein encoded by dbv gene cluster ORF17.
                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 1; 812pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 28; Page 95-112; 164pp; English.
                                                                                                    Takaishi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ŀ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5;
         07-JUN-2002; 2002JP-00167239
                                                    (SUMO ) SUMITOMO CHEM CO LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25.9%;
32.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-OCT-2002; 2002EP-00023597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Actinomadura sp. ATCC 39727.
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                                                                                                 Mukumoto
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                                                                                                                                              WPI; 2003-523102/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-332813/31
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Best Local Similarity
                                                                                                                                                                 N-PSDB, ADC36139
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                                                                                                 Nakajima H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention.
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reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in dagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders (IV) appetide and polymoleotide sequences have applications in captypeptide and polymuleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the wind the capters are sequences.
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Sequence 264 AA;

Gaps 9 Query Match 25.5%; Score 56; DB 4; Length 264; Best Local Similarity 38.7%; Pred. No. 25; Matches 12; Conservative 4; Mismatches 9; Indels

: | | :: |: || || || || 197 APQTLINPMEVREHVPRRHASQCFWVKSGRD 227 16 SPDTGLDPLTVRRHVP-----AVWVLLSRD 40

ઠે 셤 Search completed: January 26, 2005, 15:01:07 Job time : 42.861 secs

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TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRDP 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 220; DB 9; Best Local Similarity 100.0%; Pred. No. 6.2e-21; Matches 41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 459, Application US/09876997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : Homo sapiens
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US-09-731-872-459
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US-09-876-997-459
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Sequence 668, App
Sequence 432, App
Sequence 254668,
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308895,
308929,
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Sequence 308929,
Sequence 61107,
Sequence 54515,
Sequence 58679,
Sequence 60913,
Sequence 60913,
                                                                                                    January 26, 2005, 15:06:38; Search time 34.1898 Seconds (without alignments) 433.254 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          '(cgn2_6/ptodata/1/pubpaa/USO7 PUBCOMB.pep:*
'(cgn2_6/ptodata/1/pubpaa/USO5 Maw PUB.pep:*
'(cgn2_6/ptodata/1/pubpaa/USO5 Maw PUB.pep:*
'(cgn2_6/ptodata/1/pubpaa/USO5 PUBCOMB.pep:*
                                                                                                                                                                                                               1 TKLRFLQTEDSWVPASPDTG......DPLTVRRHVPAVWVLLSRDP
5.1.6
Compugen Ltd.
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US-109-978-360A-668
US-10-423-1860-432
US-10-425-115-254668
US-10-425-115-308952
US-10-425-114-61107
US-10-425-114-61107
US-10-425-114-54515
US-10-425-114-56679
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                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                          1608061 seqs, 361289386 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                    US-10-057-813-14_COPY_85_125
220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
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Match Length
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Perfect score:
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Gaps

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Length 163; Indels

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Sequence 452, Application US/09731872

Sequence 452, Application US/09731872

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Dumas Milne Edwards, Jean Baptiste

APPLICANT: Bougueleret, Lydie

APPLICANT: Bougueleret, Lydie

TITLE OF INVENTION: FULL-LENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS

FILE REFERENCE: 78.US3.REG

CURRENT APPLICATION NUMBER: US/09/731,872

CURRENT PILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 60/169,629

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR APPLICATION NUMBER: US 60/187,470

PRIOR PILING DATE: 2000-03-06

NUMBER OF SEQ ID NOS: 482

SOFTWARE PATENT.

SEQ ID NO 459

LENGTH: 163
                                                 Sequence 120370,
Sequence 2808, Ap
Sequence 203439,
Sequence 191078,
Sequence 113299,
Sequence 121340,
Sequence 121940,
Sequence 14, Appl
Sequence 14, Appl
Sequence 22955,
Sequence 22955,
Sequence 152741,
Sequence 12782,
Sequence 152741,
Sequence 152741,
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Sequence 152741,
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Sequence 1
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                                                   US-10-437-963-120370
US-10-408-765A-2808
US-10-408-765A-2808
US-10-425-115-303349
US-10-425-115-303349
US-10-425-115-319295
US-10-425-115-213299
US-10-425-115-213299
US-10-437-963-121940
US-10-369-493-14659
US-10-18-437-963-121940
US-10-424-599-225595
US-10-424-599-237821
US-10-369-493-12782
US-10-156-761-13399
US-10-128-799-42
US-10-128-799-42
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Sequence 432, Application US/10723860

| Sequence 432, Application US/10723860
| Publication No. US2004025360641
| GENERAL INFORMATION:
| APPLICANT: Aziz, Natasha
| APPLICANT: Ziotnik, Albert,
| TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
| FILE REPERENCE: 05882.0193.NPUS01
| CURRENT APPLICATION NUMBER: 05/429,739
| PRIOR PILING DATE: 2003-11-26
| PRIOR PILING DATE: 2002-11-26
| NUMBER OF SEQ ID NOS: 8393
| SOFTWARE: PatentIn version 3.2
| SEQ ID NO 432
| LEMOTH: 553
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Avain, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 254668
LENGTH: 242
                                                                                                                                                                                                                                                                                                                   Length 163;
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Pred. No. 1.7e-17;
0; Mismatches 5;
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LOCATION: (1)..(242)
OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                                                 70, 103, 107, 108)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 EDSWVPASPDIGLDPLTVRRHVPAVWVL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 EEPWVPSGTDTTLSRTTYRRNPGSWSL 84
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Publication No. US20040214272A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 87.8%;
Matches 36; Conservative
                                                                                                                                            ; NAME/KEY: misc_feature
; LOCATION: (36, 47, 54, 65,
; OTHER INFORMATION: unknown
US-09-978-360A-668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Zea mays
                                            NAME/KEY: SIGNAL
LOCATION: -52..-1
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US-10-723-860-432
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                                                                                                             FEATURE:
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                                                   APPLICANT: Dunas Milne Edwards, Jean Baptiste
APPLICANT: Bougeleret, Lydie
APPLICANT: Bougueleret, Lydie
APPLICANT: Jobert, Severin
TITLE OF INVENTION: FULL-IENGTH HUMAN CDNAS ENCODING POTENTIALLY SECRETED PROTEINS
FILE REFERENCE: 78.US4.CIP
CURRENT APPLICATION NUMBER: US 09/731,872
PRIOR PILING DATE: 2001-06-08
PRIOR PILING DATE: 2000-012-07
PRIOR APPLICATION NUMBER: US 60/187,470
PRIOR APPLICATION NUMBER: US 60/189,629
PRIOR PILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: US 60/169,629
PRIOR PILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 482
SEQ ID NO 459
LENGTH: 163
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| Sequence 666, Application US/09978360A | Sequence 666, Application No. US20040110939A1 | Sequence 666, Application No. US20040110939A1 | Sequence 668, Application No. US20040110939A1 | Sequence 668, Application No. US20040110939A1 | Sequence 668, Application Notice (Sequence 678) | Application Notice (Sequence 678) | Sequence 678 | Sequence 778 
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US20030152921A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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SOFTWARE: Patent.pm
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Best Local Similarity 43.8 Matches 14; Conservative
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Best Local Similarity
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: APPLICANT: APOWER:
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: US/10/425,115
SEQ ID NO 308929
LENGTH: 276
                                                                                                                                                                                                                                                                                                              Sequence 308895, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(53222)B
FILE REPERENCE: 38-21(53222)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 308895
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                                                                                                                             Gaps
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                                                                                 29.5%; Score 65; DB 17; Length 242; 34.1%; Pred. No. 2.8; tive 8; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.1%; Score 64; DB 17; Length 276; Best Local Similarity 43.8%; Pred..No. 4.4; Matches 14; Conservative 5; Mismatches 11; Indels
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                                                                                                                                                                                              1 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRDP 41
               ; OTHER INFORMATION: Clone ID: MRT4577_163838C.1.pep
US-10-425-115-254668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , OTHER INFORMATION: Clone ID: MRT4577_4477C.1.pep
US-10-425-115-308895
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US-10-425-115-308929
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                                                                             Query Match
Best Local Similarity 34.14
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
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ORGANISM: Zea mays
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Sequence 61107, Application US/10425114

Publication No. US2004003488A1

GENERAL INFORMATION:
APPLICANT: Liu, Jindedong
APPLICANT: Liu, Jindedong
APPLICANT: Zhou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (5313) B
CURRENT FILING DATE: 2003-04-28
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 61107
LENGTH: 301
Squence 60670, Application US/10425114

Squence 60670, Application US/10425114

Squence 60670, Application US/10425114

Squence 60670, Application US/2004003488A1

Squence 50670, Application No. US2004003488A1

Squence Maralian Ind., Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Palaska, Jack E

APPLICANT: Palaska, Jack E

APPLICANT: Palaska, Jack E

APPLICANT: Screen, Steven E

APPLICANT: Sc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Clone ID: LIB3357-033-B9_FLI.pep
US-10-425-114-60670
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US-10-425-114-61107
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RESULT 10

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APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Screen, Jack E
APPLICANT: Tabasks, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: US/10/425,114
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 60913
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43.8%; Pred. No. 5.3;
tive 5; Mismatches 11; Indels
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US-10-425-114-60913
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28.9%; Score 63.5; DB 14;
Best Local Similarity 41.0%; Pred. No. 8.5;
Matches 16; Conservative 4; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 LRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRDP
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APPLICANT: BSHIRWA, UUN
APPLICANT: BSHIRWA, HROSHI
APPLICANT: SAKAKI, VOSHIVKI
APPLICANT: SAKAKI, VOSHIVKI
APPLICANT: HATTORI, MASAHIRA
TITLE BC FINNENTION: NOVEL POLYNUCLEOTIDES
TITLE REPERBNCE: 249-262
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: US/10/156,761
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-06-30
SPIOR FILING DATE: 2001-06-30
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Applicant Shou, Yihua
APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-156-761-11365
Sequence 11365, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptomyces avermitilis
                          Zhou, Yihua
Kovalic, David K.
Screen, Steven E
Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cuery Match
Best Local Similarity 43.89
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-425-115-308917
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US-10-425-114-54515

Sequence 54515, Application US/10425114

Publication No. US20040034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Abou, Yihua

APPLICANT: Abou, Yihua

APPLICANT: Cao, Yongwei

TILE OF INVENITON: Nucleic Acid Molecules and Other Molecules Associated With

TILE OF INVENITON: Plants and Uses Thereof for Plant Improvement

TILE REFERENCE: 38-21(5313) B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 54515

LENGTH: 315
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APPLICANT: Zhou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Solation S
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29.1%; Score 64; DB 15; Length 315;
Best Local Similarity 43.8%; Pred. No. 5.1;
Matches 14; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: UC-ZMFLMO17184G05_FLI.pep
US-10-425-114-54515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: 700577207_FLI.pep
US-10-425-114-58679
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Publication No. US20040034888A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-425-114-58679
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21 (53.22) B CURRENT APPLICATION NUMBER: US/10/425,115 CURRENT FILING DATE: 2003-04-28 NUMBER: OF SEQ ID NOS: 369326 SEQ ID NO 308917 LENGTH: 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 45240, Application US/10767701
Publication No. US20040172684A1
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 45240
LENGTH: 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.2%; Score 62; DB 16; Length 275; Best Local Similarity 43.8%; Pred. No. 8; Matches 14; Conservative 4; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C7873_1.pep
US-10-767-701-45240
                                                                                                                                                                                                                             TYPE: PRT
ORCANISM: Zea mays
ORCANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(261)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: MRT4577_4479C.1.pep
US-10-425-115-308917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-767-701-45240
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Search completed: January 26, 2005, 15:28:37 Job time : 35.1898 secs

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GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION:
FILE REFERENCE:
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER:
FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER:
FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER:
CURRENT APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
CURRENT FILING DATE:
PRIOR APPLICATION NUMBER:
SEQ ID NOS: 14342
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Best Local Similarity
Matches 40; Conserv
  LOCATION: -52..-1
NAME/KEY: UNSURE
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US-09-489-039A-10912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: SIGNAL
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FEATURE:
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Sequence 10912, A
Sequence 9644, Ap
Sequence 21900, A
Sequence 12558, A
Sequence 10, Appl
Sequence 6, Appli
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Sequence 8, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1568, A
Sequence 1596, A
Sequence 1506, A
Sequence 28, Appl
Sequence 31, Appl
Sequence 31, Appl
                                                                                            January 26, 2005, 14:52:47; Search time 10.4237 Seconds (without alignments) 260.851 Million cell updates/sec
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                                                                                                                                                    US-10-057-813-14_COPY_85_125
220
1 TKLRFLQTEDSWVPASPDTG......DPLTVRRHVPAVWVLLSRDP
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-489-033A-10912
US-09-489-033A-10912
US-09-252-991A-29644
US-09-252-991A-29644
US-09-252-991A-29674
US-09-252-991A-29674
US-09-377-557-10
US-09-317-557-10
US-09-317-557-10
US-09-489-033A-13855
US-07-923-976-6
US-07-923-976-6
US-09-134-001C-4956
US-09-134-001C-495-31
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Maximum Match 1008
Listing first 45 summaries
                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Perfect score:
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No.
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              Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 26939, A
Sequence 4, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 670, Ap
Sequence 374, App
Sequence 103, Appl
Sequence 20955, A
Sequence 20955, A
Sequence 20955, A
Sequence 23, Appl
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1 Similarity 97.6%; Pred. No. 2.5e-22; 
40; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                              Sequence 4077, Application US/09621976

Batent No. 6639063;
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: JODERT, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTE and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054FRZ
CURRENT APPLICATION UNDRER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4077
LENGTH: 128
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ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Xaa = Asp, Glu, Gly, Val
US-09-621-976-4077
  TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 586

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APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS FILE REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
SEQ ID NOS: 33142
SEQ ID NO 31900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12558, Application US/09489039A
Patent No. 6610836
Patent No. 6610836
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: GATY BREED et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: NUMBER: US/094001
CURRENT APPLICATION NUMBER: US/094001
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12558
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Pred. No. 46;
1; Mismatches 17; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312 TKARHLPIDRSEORHPWVRAPGTGPASCSACSSPRPARRPTPCAW 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TKLRFLQTEDS-----WV-----PASPDTGLDPLTVRRHVPAVW 34
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APPLICANT: Falco, S. Carl
APPLICANT: Falco, Layo O.
APPLICANT: Orozco, Emil M. Jr.
TITLE OF INVENTION: Amino Acid Decarboxylases
FILE REPERENCE: BB-123.
CURRENT APPLICATION NUMBER: US/09/377,557
CURRENT FILING DATE: 1999-08-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 51.5; DE
Pred. No. 53;
4; Mismatches
                                                           Sequence 31900, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 10, Application US/09377557; Patent No. 6297055
                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CRGANISM: Klebsiella pneumoniae
US-09-489-039A-12558
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35.6%;
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23.4%;
Best Local Similarity 37.5%;
Matches 15; Conservative 4
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Best Local Similarity 35.6'
Matches 16; Conservative
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US-09-489-039A-12558
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                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 2.709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
PRIOR PILING DATE: 2000-01-27
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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                                                                                                                                                       Gaps
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS; FILE REFERENCE: 107196.136; CURRENT APPLICATION NUMBER: US 60/074,788; PRIOR APPLICATION NUMBER: US 60/074,788; PRIOR PLILING DATE: 1998-02-18; PRIOR FILING DATE: 1998-02-18; PRIOR FILING DATE: 1998-07-27; NUMBER OF SEQ ID NOS: 33142; SEQ ID NO 29674
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                                                                                                      DB 4; Length 586;
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85;
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                                                                                                                                                  13; Indels
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                                                                                         Query Match
28.0%; Score 61.5; DE
Best Local Similarity 35.7%; Pred. No. 2.9;
Matches 15; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11arity 33.3%; Score 54; DB 11arity 33.3%; Pred. No. 85; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                            Sequence 9644, Application US/09489039A Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:|::| ::||690 WLPSAPQLNVNPLTIKQQAEA 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12 WVPASPDTGLDPLTVRRHVPA 32
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 13; Conserv
                                US-09-489-039A-10912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-252-991A-29674
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                                                                                                                                                                                                                                                                                                                                      US-09-489-039A-9644
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US-09-489-039A-9644
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ALID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMIONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13855
LENGTH: 717
                  Gaps
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                  ë,
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Pred. No. 94;
3; Mismatches 12; Indels
                  9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/07923976
Patent No. 5574136
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: DNA Encoding Granulocyte
TITLE OF INVENTION: Oclony-Stimulating Factor Receptor NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: P.O. Box 2266 Eads Station
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Arington STATE: Virginia STATE: PROPOSIMEDE FORMINIA SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACTORING SYSTEM: PC-DOS/MS-DOS CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: AJS FRICK STATE S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       276 EDEWIPIRP--GTDAALV---AGIAWVLINED 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 EDSWVPASPDIGLDPLTVRRHVPAVWVLLSRD 40
            1; Mismatches
                                                                                                                                                                                                                                                  US-09-489-039A-13855
; Sequence 13855, Application US/094890339A
; Patent No. 6610836
; GENERAL INFORMATION:
                                                                                                              428 WVPEPPELGKSPLT---HYTIFW 447
                                                                           12 WVPASPDTGLDPLTVRRHVPAVW 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 23.4%;
Best Local Similarity 37.5%;
Matches 12; Conservative
               10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 10
US-07-923-976-6
               Matches
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                                                                                                                                                                                                                                                                                                              DB 3; Length 497;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/419,652
FILING DATE: 11-APR-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/248,532
FILING DATE: 13-AMY-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/94,713
FILING DATE: 19-JUL-1993
ATTORNEY/AGENT INFORMATION:

NAME: Kass, Alan P
REGISTRATION NUMBER: 32142
REFERENCE/POCKET NUMBER: 25 9174
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/08419652
Patent No. 5831007
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOffmann-La Roche Inc.
                                                                                                                                                                                                                                                                                                              Score 51.5; DE
Pred. No. 60;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51.5; I
Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jorsey
COUNTRY: United States of America
ZIP: 07110-1199
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PC Compatible
OPERATING SYSTEM: MS-DOS
EARLIER APPLICATION NUMBER: 60/099,493
EARLIER FILING DATE: September 8, 1998
NUMBER OF SEQ ID NOS: 20
SCFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     471 PLTEERHVDAAWKLL-RD 487
                                                                                                                                                                                                                                                                                                                                                                                                                               23 PLIVRRHVPAVWVLLSRD 40
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INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 602 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23.4%;
                                                                                                                                                                                                                                                                                                        Query Match 23.4%;
Best Local Similarity 66.7%;
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Region
LOCATION: 1.602
COTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
COTHER INFORMATION:
                                                                                                                                                                                TYPE: PRT
ORGANISM: Oryza sativa
US-09-377-557-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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Score 51.5; DB 1; Length 836;
Pred. No. 1.18+02;
1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Nagata, Shigekazu
APPLICANT: Nagata, Shigekazu
APPLICANT: Nagata, Shigekazu
APPLICANT: Pukunaga, Rikiro
ITILE OF INVENTION: DNA Encoding Granulocyte
ITILE OF INVENTION: Colony-Stimulating Factor Receptor
NUMBER OF SEQUENCES:
ADDRESSEB: Jones, Tullar & Cooper, P.C.
STREET: P.O. Box 2266 Eads Station
CITY: Arlington
STATE: Virginia
ZIP: 22222
COMPUTER READABLE FORM:
MEDIUM ITYPE: Floppy disk
                               SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 23-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/929/1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/1990
PRIOR APPLICATION NUMBER: US/07/1990
PRIOR APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 WVPASPDTGLDPLTVRRHVPAVW 34
                 PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 13
US-07-923-976-8
; Sequence 8, Application US/07923976
; Patent No. 5574136
                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 51.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 836 amino acida
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 43.54
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  703-415-1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-923-976-4
                   OPERATING SYSTEM:
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### APPLICATION NUMBER: 15.7329

### APPLICATION NUMBER: 15.7329

### APPLICATION NUMBER: 15.734-1993

### APPLICATION NUMBER: 15.734-1993

### APPLICATION NUMBER: 522.952

### APPLICATION NUMBER: 522.952

### APPLICATION NUMBER: 522.952

### APPLICATION NUMBER: 522.952

### APPLICATION NUMBER: 416.306

### APPLICATION NUMBER: 416.306

### APPLICATION NUMBER: 416.306

### APPLICATION NUMBER: 412.916

### APPLICATION NUMBER: 412.916
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                                                                                                                                                                                                                                                         Score 51.5; DB 1; Length 771;
Pred. No. 1e+02;
1; Mismatches 9; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51.5; DB 6; Length 783;
Pred. No. 1e+02;
1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 12
US-07-921-976-4
is Sequence 4, Application US/07923976
is Sequence 4, Application US/07923976
is Patent No. 5574136
is GENERAL INFORMATION:
is APPLICANT: Nagata, Shigekazu
is APPLICANT: Fukunaga, Rikiro
is TITLE OF INVENTION: Colony-Stimulating Factor Receptor
is NUMBER OF SEQUENCES:
is ADDRESSEE: Jones, Tullar & Cooper, P.C.
is STREET: P.O. Box 2266 Eads Station
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Jones, Tullar & Cooper, P.C. STREET: P.O. Box 2266 Eads Station CITY: Arlington STATE: Virginia ZIP: 22202 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
REFERENCE/DOCKET NUMBER: 514853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 771 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                 547 WVPEPPELGKSPLT---HYTIFW 566
                                                                                                                                                                                                                                                                                                                                        12 WVPASPDTGLDPLTVRRHVPAVW 34
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                                                                                                                                                                                                                                                       Query Match 23.4%;
Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 43.5%;
Matches 10; Conservative
                                                                                                                                                                                   ) MOLECULE TYPE: protein US-07-923-976-6
                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 783
                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO:2
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Gaps

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COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,976
FILING DATE: 19920922
CLASSIFICATION: 435
CLASSIFICATION: 435
RICA SAPLICATION DATA:
APPLICATION NUMBER: UP 74539/1990
FILING DATE: 23-MAR-1990
PRICA APPLICATION DATA:
APPLICATION NUMBER: UP 176629/1990
FILING DATE: 03-JUL-1990
PRICA APPLICATION DATA:
APPLICATION NUMBER: PCT/JP91/00375
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, Jamee W.
REGISTRATION NUMBER: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: HELLWEGE, Jamee W.
REGISTRATION NUMBER: 28-MAR-1991
TELECOMMULCATION NUMBER: 514853
TELERHONE: 010-415-1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 23.0%; Score 50.5; DB 1; Best Local Similarity 43.5%; Pred. No. 1.6e+02; Matches 10; Conservative 2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: January 26, 2005, 15:08:53
Job time : 11.4237 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 WVPASPDTGLDPLTVRRHVPAVW 34
                COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 703-415-1508
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 837 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: protein
US-07-923-976-2
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Patent No. 6380370

Patent No. 6380370

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILLE OF INVENTION: BEIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1997-08-13

PRIOR PILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674
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23.4%; Score 51.5; DB 1; Length 863;
Best Local Similarity 43.5%; Pred. No. 1.2e+02;
Matches 10; Conservative 1; Mismatches 9; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/07923976

Sequence 2, Application US/07923976

Patent No. 5574336

GENERAL INPORMATION:

APPLICANT: Nukunaga, Rikiro

TITLE OF INVENTION: DNA Encoding Granulocyte

TITLE OF INVENTION: Colony-Stimulating Factor Receptor;

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jones, Tullar & Cooper, P.C.

STREET: P.O. Box 2266 Eads Station

CITY: Arlington

STATE: Virginia

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.2%; Score 51; DB 3; Length 196; Best Local Similarity 39.0%; Pred. No. 23; Matches 16; Conservative 4; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TKLRFLQTEDSWVPASPDTGLDPLTVRRHVPAVWVLLSRDP 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547 WVPEPPELGKSPLT---HYTIFW 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-4956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 WVPASPDTGLDPLTVRRHVPAVW 34
                                                                                        514853
ATTORNEY/AGENT INFORMATION:
NAME: Hellwege, James W.
REGISTRATION UNDRER: 28,808
REFRENCE/DOCKET UNDRER: 51485
TELECOMMUNICATION INFORMATION:
TELEFAX: 703-415-1500
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 863 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                       , MOLECULE TYPE: protein US-07-923-976-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 14
US-09-134-001C-4956
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LENGTH: 196
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US-07-923-976-2
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January 26, 2005, 15:44:05; Search time 39 Seconds (without alignments) 101.151 Million cell updates/sec
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220
1 TKLRFLQTEDSWVPASPDTG......DPLTVRRHVPAVWVLLSRDP
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

Minimum DB seq length: 0 Maximum DB seq length: 41

pollen allergen phe Mallikrein - mouse procathepsin L - g trypsin inhibitor hypothetical prote Ig heavy chain V r lg keavy chai probable transposa hypothetical prote Ig heavy chain v r light-harvesting p photosystem I 1igh photosystem I 22K glue protein - rib photosystem I ligh photosystem I ligh myosin - human (fr Ig heavy chain V r Ig heavy chain V r hypothetical prote neutral phosphatas T-cell receptor be mers protein homol photosystem I prot Description SUMMARIES T36994 H84214 LBRRG74 G45095 S03275 A61075 F45095 E45095 I61698 S03275 T70022 T70022 S68341 S68341 S68341 S46472 JN0252 T29628 S46469 S26937 G69471 I70018 **S**55462 B % Query Match Length I Score 32 31.5 31.5 31 31 31 31 30.5 33 33 32.5 32 Result No.

hypothetical prote histone H3 homolog	hypothetical prote thypothetical prote thyrotropin-releas inalinalike order	apolipoprotein Cbi agglutinin - Japan serine proteinase	trypein inhibitor dopamine D3 recept hypothetical prote cytochrome c(EDH)	hypothetical EWSR1 homeobox 4 protein antifreeze glycopr
A86127 T28154	G82685 AH2787 A45096 A54651	S67974 S30375 JX0059	JX0058 165220 D82691 S29766	151887 JC2059 B25213
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ALIGNMENTS

RESULT 1

9448

#3.600ut 1	
ction 1 [imported] -	- Streptomyces coelicolor (fragmen
C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 15-Sep-2000	text_change 15-Sep-2000
ll, J.; Barrell,	.; Barrell, B.G.; Rajandream, M.A.
A; Accession: T36994	
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	
A;Residues: 1-36 <oli> A;Cross-references: EMBL:AL109949; PIDN:CAB52908.1; GSPDB:GN00070; SCOEDB:SCJ11.23c</oli>	3SPDB:GN00070; SCOEDB:SCJ11.23c
A,Experimental source: strain A3(2) C,Genetics:	
A;Gene: SCOEDB:SCJ11.23c C;Superfamily: Streptomyces coelicolor probable transposase SC6G9.06c	вроваве SC6G9.06c
Query Match 18.2%; Score 40; DB 2; Length 36; Best Local Similarity 40.6%; Pred. No. 1.2e+02; Matches 13; Conservative 3; Mismatches 8; Indels 8;	ingth 36; Indela
Qy 8 TEDSWVPASPDTGLDPLIVRRHVPAV 33	
Db 2 SEPSWTAPFTGLSPRCSWKLVTVLRRQGAV 31	
RESULT 2 H84214	
hypothetical protein Vng0570h [imported] - Halobacterium sp. NRC-1	rium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004	text_change 09-Jul-2004
Ring, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky,	B.; Pan, M.; Shukla, H.D.; Lasky,
; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Me Jung, K.H.; Alam, M.; Freitas, T.	; Hough, D.W.; Maddocks, D.G.; Jabl
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000	
A.Authors: Hou, S.; Daniels, C.J.; Dennis, P.F.; Omer, A.D.; Ednardt, H.; Lowe, I.M.; A,Title: Genome sequence of Halobacterium species NRC-1.	C-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950 A;Accession: H84214	5950
A, Status: preliminary	
A;Cross-references: UNIPROT:Q9HRS4; GB:AE004437; NID:g10580164; PIDN: C:Genetics:	:g10580164; PIDN:AAG19084.1; GSPDB ·
A; Gene: VNGO570H	
16.8%;	Length 35;
les 7; Conservative 2	Indels

Gaps

11;

Length 38; Indels

7

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glue protein - ribbed mussel (fragments)
C;Species: Geukensia demissa (ribbed mussel)
C;Date: 03.Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C;Accession: A61077
R;Waite, J.H.; Hansen, D.C.; Little, K.T.
R;Waite, J.H.; Hansen, D.C.; Little, K.T.
A;Title: The glue protein of ribbed mussels (Geukensia demissa): a natural adhesive with A;Reference number: A61077; MUID:90110595; PMID:2481690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C. Accession: 803275
R. Murata, N.; Kajiura, H.; Fujimura, Y.; Miyao, M.; Murata, T.; Watanabe, A.; Shinozaki Prog. Photosyn. Res. 1, 701-704, 1987
A. Title: Partial amino acid sequences of the proteins of pea and spinach photosystem II A; Reference number: 803269
A. Accession: 803275
A. Accession: 803275
A. Accession: 803275
A. Molecule type: protein
A; Residues: 1-25 cMUR>
C; Superfamily: chlorophyll a/b-binding protein
C; Keywords: chloroplast; photosynthesis; photosystem II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     photosystem II 22K protein - spinach (fragment)
C;Species: Spinacia oleracea (spinach)
C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 21-Aug-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.9%; Score 35; DB 2; Length 25; 53.3%; Pred. No. 3.7e+02; tive 1; Mismatches 4; Indels
A;Regidues: 1-38 <BAS>
A;Cross-references: UnPROT:Q9S8T9
A;Note: sequence extracted from NCBI backbone (NCBIP:120940)
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: chloroplast; thylakoid
                                                                                                                                                                                                                                                                                                                                                                                    5e+02;
                                                                                                                                                                                                                                                                                                                  Query Match 16.1%; Score 35.5; DB Best Local Similarity 33.3%; Pred. No. 5e+02; Matches 9; Conservative 4; Mismatches
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C;Superfamily: glutenin
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Nature Genet. 7. 162-168, 1994

Nature Genet. 846474

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Nate Genet. 846474

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National Research 84774

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Cibate: 04-Dec:1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
Cibatession: A03455
Bibl. Chem. Hoppe-Seyler 366, 87-98, 1985
A;Title: The light-harvesting polypeptides of Rhodopseudomonas viridis. The complete ami A;Reference number: A90694; MUID:85225948; PMID:3890891
A;Accession: A03455
A;Molecule type: protein
A;Kesidues: 1.36 e.BRU>
A;Cross-references: UNIPROT:P04126
A;Cross-references: UNIPROT:P04126
A;Cross-references: UNIPROT:P04126
C;Superfamily: light-harvesting protein gamma chain
C;Keywords: antenna complex; bacteriochlorophyll; membrane protein
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G45095
photosystem I light-harvesting complex chlorophyll a/b protein p22.1/p22 - Chlamydomonas C;Species: Chlamydomonas reinhardtii
C;Becies: Chamydomonas reinhardtii
C;Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: G5095
R;Bassi, R.; Soen, S.Y.; Frank, G; Zuber, H.; Rochaix, J.D.
J. Biol. Chem. 267, 25714-25721, 1992
A;Title: Characterization of chlorophyll a/b proteins of photosystem I from Chlamydomona A;Reference number: A45095; MUID: 93100280; PMID: 1464588
A;Accession: G45095
A;Status: preliminary
A;Molecule type: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Homo sapiens (man)
Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ight-harvesting protein B-1015 gamma chain - Rhodopseudomonas viridis Species: Rhodopseudomonas viridis Jate: 04-Dec-1986 #sequence_revision 04-Dec-1986 #s
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16.4%; Score 36; DB 1; Length 36;
Best Local Similarity 28.6%; Pred. No. 4.1e+02;
Matches 10; Conservative 8; Mismatches 15; Indels
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                                ASPDTGLDPLTVRRH 29
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Gaps

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C.Keywords: hydroxylysine; hydroxyproline; tandem repeat
C.Keywords: hydroxylysine; a.4.-dihydroxyphenylalanine (Tyr) #status experimental
F;3,7,12,21/Modified site: 4-hydroxyproline (Pro) #status experimental
F;16,30,34/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) (partial) #status experimen
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                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                  Length 35;
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30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

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R;Matthiesen, F.; Lowenstein, H.
Clin. Exp. Allergy 21, 297-307, 1991
A;Title: Group V allergens in grass pollens. I. Purification and characterization of th
A;Reference number: A61505; MUID:91322736; PMID:1863892
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                                                                                                                                         C;Species: Zea maye (maize)
C;Species: Zea maye (maize)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
C;Accession: S1461
R;Kangasjarvi, J.; Gengenbach, B.G.
R;Kangasjarvi, J.; Gengenbach, B.G.
A;Description: Nucleotide sequence of maize plastid genome BamHI 14 fragment.
A;Reference number: S14660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Mus musculus (house mouse)
C;Dacester: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999
C;Accession: 170022
R;Evans, B.A.; Drinkwater, C.C.; Richards, R.I.
J; Biol. Chem. 262, 8027-8034, 1987
A;Tille: Mouse glandular kallikrein genes: Structure and partial sequence an A;Reference number: 155260; MUID:87250386; PMID:3036794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pollen allergen Phl p V - common timothy (fragment)
C;Species: Phleum pratense (common timothy)
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C;Accession: A61505
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A Molecule type: protein
A;Residues: 1-24 <MAT.
A;Cross-references: UNIPROT: Q7MIL8
A;Cross-references: UNIPROT: Q7MIL8
A;Note: 2-Ala, 5-Gly, and 15-Glu were also found
C;Superfamily: grass pollen allergen IX
C;Reywords: hydroxyproline; pollen
C;Reywords: hydroxyproline; pollen
F;6,9,12,18,21,24/Modified site: hydroxyproline (Pro) #status experimental
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A,Status: preliminary
A,Mosideule type: DNA
A,Residues: 1-18 <KAN>
A,Cross-references: EMBL:X58080; NID:g12429; PIDN:CAA41109.1; PID:g12431
C,Superfamily: photosystem I P700 apoprotein
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A;Gene: KAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 2; Length 18;
Pred. No. 4.7e+02;
4; Mismatches 8; Indels
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A;Molecule type: DNA
A;Residues: 1-38 <RES>
                                                                                                           - maize (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 LTVRRHVPAVWVLLSRDP 41
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Best Local Similarity 33.3%;
Matches 6; Conservative
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Best Local Similarity 50.0
Matches 6; Conservative
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                                                                                                           photosystem I protein psaA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A, Accession: A61505
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Cipate: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
Cipate: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
Cipate: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
Ribassion: 86.7 5095
Giber, R.; Soen, S.Y.; Frank, G.; Zuber, H.; Rochaix, J.D.
J. Biol. Chem. 267, 25714-25721, 1992
A; Fitle: Characterization of chlorophyll a/b proteins of photosystem I from Chlamydomona A; Reference number: A45095; MUID:93100280; PMID:1464588
A; Accession: B45095
A; Accession: B45095
A; Residues: 1-30 <ABS>
A; Residues: 1-30 <ABS>
A; Residues: 1-30 <ABS>
A; Cross-references: UNIDROT:09S8U1
A; Note: sequence extracted from NBI backbone (NCBIP:120937)
C; Superfamily: chlorophyll a/b-binding protein
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Proc. Natl. Acad. Sci. U.S.A. 91, 6549-6553, 1994

A; Title: Identification and overlapping expression of multiple unconventional myosin gen

A; Reference number: A55758; MUID:94294418; PMID:8022818

A; Recession: I61698

A; Accession: I61698

A; Accession: Dreliminary; translated from GB/EMBL/DDBJ

A; Residues: I-31 cRES

A; Cross-references: UNIPROT:Q14786; GB:L29147; NID:9457255; PIDN:AAA20910.1; PID:9531140
C; Accession: F45095
R; Bassi, R.; Soen, S.Y.; Frank, G.; Zuber, H.; Rochaix, J.D.
J. Biol. Chem. 257, 25714-25721, 1992
A; Title: Characterization of chlorophyll a/b proteins of photosystem I from Chlamydomona A; Reference number: A45095; MUID:93100280; PMID:1464588
A; Recession: F45095
A; Rocession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  notosystem I light-harvesting complex chlorophyll a/b protein p18.1 - Chlamydomonas rei
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50.0%; Pred. No. 7.3e+02;
tive 3; Mismatches 1; Indels
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15.2%; Score 33.5; DB 2;
Best Local Similarity 33.3%; Pred. No. 7e+02;
Matches 8; Conservative 1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / Match 15.5%; Score 34; DB 2; I Local Similarity 28.3%; Pred. No. 8.3e+02; les 13; Conservative 2; Mismatches 5.
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Matches 7; Conserv
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Crypsin inhibitor A - balsam pear Cispedies: Momordica charatia (balsam pear, bitter gourd)
Cispedies: Momordica charatia (balsam pear, bitter gourd)
Cidate: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
Cidatesion: 820393
RiHuang, Q.; Liu, S.; Tang, Y.; Zeng, F.; Qian, R.
RiHuang, Q.; Liu, S.; Tang, Y.; Zeng, F.; Qian, R.
A;Hitle: Amino acid sequencing of a trypsin inhibitor by refined 1.6 A X-ray crystal str
                                                                                                                                                                                                                                                                               procathepsin L - guinea pig (fragments)
(species: Cavia porcellus (guinea pig)
(c)Species: Cavia porcellus (guinea pig)
(c)Accession: 868341
R;McDonald, J.K.; Emerick, J.M.C.
R;McDonald, J.K.; Emerick, J.M.C.
A;Title: Purification and characterization of procathepsin L, a self-processing zymogen
A;Reference number: 868341; MUID:96063618; PMID:7487106
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Query Match
14.8%; Score 32.5; DB 2; Length 38;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 8; Conservative 3; Mismatches 4; Indels
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14.5%; Score 32; DB 2; Length 28;
Best Local Similarity 38.5%; Pred. No. 1e+03;
Matches 5; Conservative 3; Mismatches 5; Indels
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Pred. No. 7.1e+02;
2; Mismatches 4;
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A,Molecule type: protein
A,Residues: 1-28 «HUA»
C,COSS-references: UNIPROT: P30709
C,Superfamily: squash trypsin inhibitor ITD I
                                                                                                                                     |: ||||| | :|:
11 LEDLTVRRIPNPGMWL 26
                                                                                                       21 LDPLTVRR-HVPAVWV 35
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Best Local Similarity 53.8%;
Matches 7; Conservative
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-11;12-20 <MCD>
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Search completed: January 26, 2005, 15:53:55 Job time : 40 secs

1 RSCPRIWMECTRD 13

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coprinus ci equus cabal sús scrofa 15 sus scrof homo sapien mycobacteri salmonella Bynechococc mycobacteri clostridium

salmonella

Q8tg83 88c Q988t8 chl Q988t8 chl Q8wide eq Q8wide eq Q8wide hor Q8vid my Q8vit em Q8

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PubMed=15024419;
PubMed=15024419;
PubMed=15024419;
PubM. Sun L.V., Vamathevan J.J., Riegler M., DeBoy R.T.,
Brownlie J.C., McGraw E.A., Martin W., Esser C., Ahmadinejad N.,
Wiegand C., Madupu R., Beanan M.J., Brinkac L.M., Daugherty S.C.,
Durkin A.S., Kolonay J.F., Nelson W.C., Mohamoud Y., Lee P.,
Berry K.J., Young M.B., Utterback T.R., Weidman J.F., Nierman W.C.,
Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.L., Eisen J.A.;
"Phylogenomics of the reproductive parasite Wolbachia pipientis wMel:
a streamlined genome overrun by mobile genetic elements.";
PLOS Biol. 2:327-341(2004).
TIGR; WD0747;
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AAS14438;
02-MAR-2004 (TrEWBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
13-APR-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
W0DA77.
Wolbachia pipientis wMel.
Bacteria, Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Wolbachieae; Wolbachia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wolbachia pipientis wMel.
Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales;
Rickettsiaceae; Wolbachieae; Wolbachia.
NCBI_TaxID=66077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protecome; Hypothetical protein.
37 AA; 4177 MW; F62611BC059D7523 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47.5; DE Pred. No. 70; 6; Mismatches
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Similarity 38.7%;
12; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
OrderedLocusNames=WD0747;
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             Local Similarity
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SEQUENCE FROM N.A
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Aas14438 wolbachia
Q8ng01 homo sapien
Q8nkn1 mycobacteri
Q6ld88 oryctolagus
Q6ld88 oryctolagus
Q5ch7 semiliquida
Q95ch7 semiliquida
Q95ch3 altingia gr
Q95ch3 altingia gr
Q95ch3 altingia ob
Q8bur6 strephonema
Q8bur6 strephonema
Q94p09 altingia ob
Q95cg3 mytilaria 1
Q95cg3 mytilaria 1
Q95cg3 mltingia ch
Q95cg3 altingia ch
Q95ch1 liquidambar
Q95ch3 laltingia ex
Q7c11 oreochromis
Q95ch3 altingia ex
Q95ch3 laltingia ex
Q10ch1 liquidambar
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(c) 1993 - 2005
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Q95CH7
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2: uniprot_trembl:*
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MEDLINE=22430160; PubMed=12534463;

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Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,

Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,

Madupu R., Melson W.C., White O., Peterson J.D., Khouri H.M.,

Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,

Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,

Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,

Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CDC 1551 / Oshkosh;
MEDLINE=22206494; Pubmed=12218036;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Fleischmann R.D., DeBoy R.T., Dodson R.J., Gwinn M.L., Haft D.H.,
Hickey E.K., Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D.,
Salzberg S.L., Delcher A., Utterback T.R., Weidman J.F., Khouri H.M.,
Eraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Whole-genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                               "Complete genome sequence and comparative analysis of the metabolically versatile Pseudomonas putida KT2440."; Environ. Microbiol. 4:799-808(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Indels
                                                                                                                                                                                                                                                                                                                                             Complete proteome; Hypothetical protein.
SEQUENCE 32 AA; 3670 MW; 726C26BA63E78739 CRC64;
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Last annotation update)
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Pred. No. 8.1e+02;
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Pred. No. 8.1e+02;
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EMBL, AE006939; AAK44547.1; -.
TIGR; MT0325; -.
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SEQUENCE 32 AA; 3683 MW;
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13 WAPATVDTAFRPM 25
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   Wu M. Sun L.V., Vamathevan J.J., Riegler M., DeBoy R.T.,
Brownlie J.C., McGraw E.A., Martin W., Esser C., Ahmadinejad N.,
Wiegand C., Mcdupu R.A., Beanan M.J., Brinkac L.M., Daudherty S.C.,
Durkin A.S., Kolonay J.E., Nelson W.C., Mohamoud Y., Lee P.,
Berry K.J., Young M.B., Utterback T.R., Weidman J.F., Nierman W.C.,
Paulsen I.T., Nelson K.E., Tettelin H., O'Neill S.L., Eisen J.A.;
"Phylogenomics of the reproductive parasite Wolbachia pipientis wMel:
plus Blol. 2:37-341(2004).
TIGR; WD0747; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
                                                                                                                                                                                                                                                                                 DB 2; Length 37;
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 32;
                                                                                                                                                                                                                                       37 AA; 4177 MW; F62611BC059D7523 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 AA; 3364 MW; 7ECF2F2138B35CC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
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Last annotation update)
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EMBL; AF331838; AAM63959.1; -.
GO; GO:0004872; F:receptor activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39; DB 2; I
Pred. No. 8.1e+02;
                                                                                                                                                                                                                                                                                                   Pred. No. 70;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                       6 LQTEDSWVPASPDTGLDPLTVRRHVPAVWVL 36
                                                                                                                                                                                                                                                                                                                                                                               32 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                               Score 47.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     muscarinic receptor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=21855767; PubMed=11867338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                               21.6%;
38.7%;
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36.8%;
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Best Local Similarity 36.88,
7; Conservative
                                                                                                                                                                                                                                                                                               Local Similarity 38.7 tes 12; Conservative
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                                                                                                                                                                                                                     Hypothetical protein.
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Q88LG0;
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Q8NG01;
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Matches
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                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledona; core eudicots; Saxifragales; Hamamelidaceae; Semiliquidambar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Saxifragales; Altingiaceae; Altingia.
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Chloroplaat.
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                  Wen J.;
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                                                                                                                                                                                                                                Score 38; DB 2; Length 24;
Pred. No. 7.9e+02;
7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17.3%; Score 38; DB 2; Length 24; 38.9%; Pred. No. 7.9e+02; tive 4; Mismatches 7; Indels
                                                                                                               SEQUENCE FROM N.A. Shang Q., Boufford D.E., Parks C.R., W Shi S., Huang Y., Zhang Q., Boufford D.E., Parks C.R., W Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF304536, AAL13187.1; - GO; GO:0009507; C:chloroplast; IEA.
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24 AA; 2812 MW; 84E1CC186B6377E3 CRC64;
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Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                               17.3%;
                 Semiliquidambar cathayensis.
Chloroplast.
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                                                                                                                                                                                                                                                            Local Similarity 38.9
1es 7; Conservative
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                                                                                                                                                                                        Chloroplast.
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SEQUENCE
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Matches
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Q95CI1
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Q95CH9
    STW RR RR SOCCOS
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TISSUE-faat twitch muscle;
MEDLINE-88169602; PubMed=2965149;
Korczak B., Zarain-Herzberg A., Brandl C.J., Ingles C.J., Green N.M.,
MacLennan D.H.;
                                                                                                                                                 TISSUE=Fast twitch muscle;
MEDLINE=88169602; PubMed=2965149;
Korczak B., Zarain-Herzberg A., Brandl C.J., Ingles C.J., Green N.M.,
MacLennan D.H.;
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                     Ca2+ ArPase (Fragment).
Oydcolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ca2+ ArPase (Fragment).
Oryccolagus cuniculus (Rabbit).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Lagomorpha; Leporidae; Oryctolagus.
                                                                                                                                                                                                    MacLennan D.H.;
"Structure of the rabbit fast-twitch skeletal muscle Ca2+-ATPase
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Pred. No. 1e+03;
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           05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMA311/2;
DO TO TEMBLICAL 27, Created)
02-MAR-2004 (TrEMBLICAL 27, Last sequence update)
02-MAR-2004 (TrEMBLICAL 27, Last annotation update)
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Last sequence update)
Last annotation update)
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TEECLAYFGVSETTGLTPDQVKRHL 33
                                                                                                                                                                                                                         J. Biol. Chem. 263:4813-4819(1988).
EMBL; M20531; AAA31172.1; -.
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EMBL; M20531; AAA31172.1; -.
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40.0%;
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 40.0°
Matches 10; Conservative
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                                                                                                                                        SEQUENCE FROM N.A.
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Q95CH7;
01-DEC-2001
01-DEC-2001
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Q95CH7
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MEDLINE-22466955; PubMed=12579451;
MEDLINE-22466955; PubMed=12579451;
Tan F., Shi S., Zhong Y., Gong X., Wang Y.;
"Phylogenetic relationships of Combretoideae (Combretaceae) inferred from plastid, nuclear gene and spacer sequences.";
J. Plant Res. 115:475-481(2002)
EMBL; AF508245; AAP29779.1;
GO; GO:0009507; C:chloroplast; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; Myrtales; Combretaceae; Strephonema.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Saxifragales; Altingiaceae; Altingia.
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Shi S., Huang Y., Zhang Q., Boufford D.E., Parks C.R., Wen J.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF304540; AAL13195.1; -.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Photosystem I P700 chlorophyll A apoprotein Al (Fragment).
                                                                                                                                                       Score 37; DB 2; Length 21;
Pred. No. 9.3e+02;
7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.8%; Score 37; DB 2; Length 21; 38.9%; Pred. No. 9.3e+02;
                                                                                                                                 B3EB6377E3A17FE6 CRC64;
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Last sequence update)
Last annotation update)
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                               EMBL; AF508246; AAP29780.1; -. GO: GO:0009507; C:chloroplast; IEA
                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
              J. Plant Res. 115:475-481(2002).
                                                                                                                                                                                                                                                                                                     24 LTVRRHVPAVWVLLSRDP 41
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21 AA; 2436 MW;
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MITRSPEPEVKILVDRDP
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01-DEC-2001 (TrEMBLrel. 19,
05-JUL-2004 (TrEMBLrel. 27,
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                                                                                                                                                                                                   Local Similarity 38.9 tes 7; Conservative
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Tan F., Shi S., Zhong Y., Gong X., Wang Y.;
"Phylogenetic relationships of Combretoideae (Combretaceae) inferred
from plastid, nuclear gene and spacer sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, Myrtales, Combretaceae, Strephonema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
                                                                                                                                                                                                                                                                                                                                       ö
                                                                                          Shi S., Huang Y., Zhang Q., Boufford D.E., Parks C.R., Wen J.; Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL, AF304534; AAL13183.1; -.. GO; GO:0009507; C:chloroplast; IEA.
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17.0%; Score 37.5; DB 2; Length 26;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 9; Conservative 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                 Score 38; DB 2; Length 24;
Pred. No. 7.9e+02;
4; Mismatches 7; Indels
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Photosystem I P700 chlorophyll A apoprotein Al (Fragment)
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF040884; AAB95609.1;
                                                                                                                                                                                                                                          84E1CC186B6377E3 CRC64;
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Last annotation update)
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Saxifragales; Altingiaceae; Altingia.
NCBI_TaxID=159571;
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24 AA; 2812 MW;
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Best Local Similarity 38.9%;
Matches 7; Conservative
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26 AA; 2956 MW;
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Hepatitis C virus.
                                                                    SEQUENCE FROM N.A.
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Mytilaria laosensis.
Chloroplast.
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Saxifragales; Hamamelidaceae; Mytilaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             [1] --
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUDMITTED (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF304544; AAL13203.1; --
GO; GO:0009507; C:chloroplast; IEA.
                                                                                        Query Match

16.8%; Score 37; DB 2; Length 24;
Best Local Similarity 38.9%; Pred. No. 1.1e+03;
Matches 7; Conservative 4; Mismatches 7; Indels
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Best Local Similarity 38.9%; Pred. No. 1.1e+03;
Matches 7; Conservative 4; Mismatches 7; Indels
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24 24 24 SEQÜENCE 24 AA; 2799 MW; 84EIC2C3EB6377E3 CRC64;
EMBL; AF304541; AAL13197.1; -. GO; GO: 0009507; C: chloroplast; IEA. Chloroplast 24 24 SEQÜENCE 24 AA; 2799 MW; 84EIC2C3EB6377E3 CRC64;
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OSSCGS;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-UN-2003 (TrEMBLrel. 24, Last senotation update)
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Search completed: January 26, 2005, 15:53:20 Job time : 204 secs

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Compugen Ltd.
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version -
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The invention relates to the isolation of genes AAC96900-C96947 encoding the human secreted proteins AAB52104-B52150. This sequence represents a fragment of the protein encoded by the gene given in the descriptor line. The sequence is used as a query sequence for doing BLASTX searches to determine homologous sequence to the protein. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins,

Claim 11; Page 439; 478pp; English.

Aam65230 Human bra	Abg59572 Human liv	Abg46955 Human pep	Aam94835 Human rep	Aab44942 Human sec	Adk01949 Hepatitis	Abb53187 Human ORF	Aar13378 Adult T-c	Aar69694 Hepatitis	Aar89566 Hepatitis	Aay98841 HLA class	1 Herz	Aag88332 HER2/NEU	Aab68622 HER-2 B C	Adh39946 Inhibitor	Aam14155 Peptide #	Aam92083 Human dig	Abb33102 Peptide #	Aam26563 Peptide #	Abb27928 Human pep
AAM65230	ABG59572	ABG46955	AAM94835	AAB44942	ADK01949	ABB53187	AAR13378	AAR69694	AAR89566	AAY98841	AAG89011	AAG88332	AAB68622	ADH39946	AAM14155	AAM92083	ABB33102	AAM26563	ABB27928
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18.2	18.2	18.2	18.2	17.7	17.7	17.7	17.5	17.5	17.5	17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.3	17.3
40	40	40	40	39	39	39	æ	38.5	е Э	38		38	38	38	38		38	38	38
56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabletic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidocterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid molecules encoding human secreted proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
                                                                                               Human secreted protein encoded by cDNA #36.
                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Ruben SM, Komatsoulis G;
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                      AAB52138 standard; peptide; 37
                                                                                                                                                                                                                                                                                             09-APR-1999; 99US-0128700P.
20-JAN-2000; 2000US-0176930P.
                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                     06-APR-2000; 2000WO-US008980.
                                                                      (first entry)
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                                                                                                                                                                                               Ното варіепв
                                                                      22-FEB-2001
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                                               AAB52138;
RESULT 1
            AAB52136
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antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, theumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; nootropic; neuroprotective; cytostatic; virucide; dermatological; immunosuppressive; antiinflammatory; anti-HIV; vulnerary; antibacterial; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; infection; vaccine; cardiovascular disorder; neurological disease; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human secreted proteins encoded by genes contained in cDNA clones (e.g. HGCAC19), useful for preventing, treating or diagnosing e.g. AIDS, multiple sclerosis, herpes virus, leukemia, tick-borne encephalitis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 37;
22;
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Pred. No.
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12-SEP-2001; 2001US-00950082.
12-SEP-2001; 2001US-00950083.
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72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 72.7
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                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37 AA;
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The invention relates to novel human genes (ABZ66891-ABZ68209) and the encoded secreted proteins (ABP99470-ABP99872) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of:

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(a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; secreted protein; cancer; tumour; hyperproliferative disorder; autoimmune disorder; inflammation; angiogenic diseases; AIDS; acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing; drug screening; chromosome identification; chromosome mapping; cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV; antianaemic; vulnerary; chromosome 3p21.31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene 359-encoded secreted protein HTXMZ07, SEQ ID NO:786.
                                                                                                                                                                                                                                                                                                                                                                                        Score 49; DB 6; Length 37;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABR01305 standard; peptide; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-MAR-2001; 2001US-0278650P.
12-SEP-2001; 2001US-00950082.
12-SEP-2001; 2001US-00950083.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 VRRHVPAVWVL 36
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3 LRRHFPALWVL 13
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                            Sequence 37 AA;
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ABR01305
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fragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing or treating cancers or other hyperproliferative disorders. Additionally, the secreted proteins and their nucleic acids may also be used in the treatment of autoimmune disorders, inflammatory disorders, diseases involving angiogenesis, AIDS (acquired immunodeficiency syndrome), hepatitis, anaemia, and to promote wound healing. Nucleic acids of the invention may be used for chromosome identification, chromosome mapping, in gene therapy, for identifying individuals from minute biological samples, as hybridisation probes, and secreted protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises the amino acid and coding sequence of human secreted proteins. The DNA and protein sequences of the invention are useful in the treatment of cardiovascular disorders, such as: arrhythmia, artherosclerosis, stroke, endocarditis, congestive heart failure, rheumatic heart disease, cardiomyopathy, haemorrhoids, varicose veins, migraine, or thrombosis. The DNA and protein sequences may also be used for treating or preventing: neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human; secreted protein; cardiovascular disorder; arrhythmia; atherosclerosis; stroke; endocarditis; congestive heart failure; rheumatic heart disease; cardiomyopathy; haemorrholds; varicose veins; migraine; thrombosis; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; renal disorder; proliferative disorder; cancer.
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diagnosing, preventing, prognosticating or treating cardiovascular
disorders (e.g. arrhythmia, atherosclerosis, cardiomyopathy, or
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                                                                                                                                                                                                                                                                                          DB 6; Length 37;
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2; Mismatches
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                                                                                                                                                                                                                                                                                      22.3%; Score 49; 72.7%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human secreted protein sequence #222.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA98381 standard; protein; 37 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-MAR-2001; 2001US-0278650P.
12-SEP-2001; 2001US-00950082.
12-SEP-2001; 2001US-00950083.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                              Conservative
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3 LRRHFPALWVL 13
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                                                                                                                                                                                                                                                                                                      Local Similarity
les 8; Conserv
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                                                                                                                                                                                                                                                  Sequence 37 AA;
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Matches
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The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide expression, comprising any of the 27,400 fully defined nucleotide acquences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expression (comprising a plurality of probes for measuring human cells or tissues. Also included are a spatially-capters of single exon nucleic acid probes cited above, where each of the plurality of probes is separately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a method of exon microarray for measuring human gene expression, a vector comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid so fer any of the above- mentioned amino acid so fer any of the above- mentioned amino acid so fer any of the above- mentioned amino acid so fer any of the above- mentioned amino acid so fer any of the above- mentioned amino acid so fer any of the above- mentioned amino acid so sequences (optionally with conservative amino acid substitutions), and isolated antibody that binds specifically to a peptide cited above, methods of selling and/or licensing single exon probes or microarrays to a customer desiring to measure gene expression, a method of providing
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pulmonary disorders, renal disorders, proliferative disorders and/or
cancerous diseases. The present amino acid sequence represents a human
secreted protein of the invention. NOTE: The present sequence is shown on
the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.
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                                                                                                                                                Length 37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   derived single exon protein #1876.
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                                                                                                                                              DB 22;
                                                                                                                                                                                         2; Mismatches
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                                                                                                                                              Score 49;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                          ABO55642 standard; protein; 40 AA.
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                                                                                                                                                22.3%;
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                                                                                                                                                                                         8; Conservative
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(RANK/) RANK D R.
(HANZ/) HANZEL D K.
                                                                                                                                                                    Best Local Similarity
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                                                                                                        Sequence 37 AA;
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99US-0137724P.
99US-0138094P.
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990S-0139119P.
990S-0139452P.
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99US-0141842P.
99US-0142154P.
99US-0142055P.
99US-0142803P.
99US-0142803P.
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99US-0143642P-
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99US-014432B-
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14-MAY-1999
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17-JUN-1999
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              human gene expression data by subscription, and a computer-readable storage medium which contains a database having a plurality of records (each record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes and apparatus are useful in gene expression analysis. The probes may be used as tools for surveying tissues to detect the presence of expressed messages that contain their specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alternative splicing events, in detecting and characterising gross alternative splicing exones, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human this patent did not form part of the invention. Note: The sequence data for this patent did not form at directly from USPTO at sequence in the sequence obtained in electronic format directly from USPTO at sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein identification, signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                       Query Match 22.0%; Score 48.5; DB 8; Length 40; Best Local Similarity 55.0%; Pred. No. 29; Matches 11; Conservative 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 73511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG57081 standard; protein; 34 AA.
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18 WLFASAD-NLDPLTLRPNTP 36
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990S-0126264P.
990S-0126785P.
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99US-0128714P.
99US-0129845P.
99US-0130077P.
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99US-0130510P.
99US-0130891P.
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08-APR-1999;
16-APR-1999;
19-APR-1999;
21-APR-1999;
23-APR-1999;
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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990S-0147204P

990S-0147303P

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990S-015408P

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990S-0155339P

990S-0153330P

990S-0159331P

990S-0159331P
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27 - JUL - 1999;
28 - JUL - 1999;
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03 - ANG- 1999;
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22 - ANG- 1999;
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21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
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                                                                                                                                                                                                                            Length 34;
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                                                                                                                                                                                                                          Score 45; DB 3;
Pred. No. 74;
1; Mismatches
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24 FEB-2000; 2000US-0186658P.
26 FAR. 2000; 2000US-0186350P.
16 MAR. 2000; 2000US-0189374P.
17 MAR. 2000; 2000US-0198123P.
19 MAY 2000; 2000US-0209467P.
26 JUN -2000; 2000US-0209467P.
30 JUL -2000; 2000US-021513P.
30 JUL -2000; 2000US-0216880P.
31 JUL -2000; 2000US-0216880P.
31 JUL -2000; 2000US-0216880P.
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36 JUL -2000; 2000US-0216880P.
37 JUL -2000; 2000US-0216880P.
38 JUL -2000; 2000US-0218290P.
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31 AUG-2000; 2000US-0225214P.
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31 AUG-2000; 2000US-0225214P.
31 AUG-2000; 2000US-0225266P.
31 AUG-2000; 2000US-0225266P.
31 AUG-2000; 2000US-0225266P.
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99US-0161405P.
99US-0161359P.
99US-0161360P.
99US-0161361P.
99US-0161920P.
99US-0161922P.
99US-0161932P.
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2000US-0225757P.
2000US-0225758P.
2000US-0225759P.
2000US-0225759P.
99US-0160989P
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Best Local Similarity 55.6%;
Matches 10; Conservative
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14-AUG-2000; 2
18-AUG-2000; 2
               25-OCT-1999,
25-OCT-1999,
26-OCT-1999,
26-OCT-1999,
26-OCT-1999,
28-OCT-1999,
28-OCT-1999,
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2000US-02320B0P.
2000US-023196BP.
2000US-023196BP.
2000US-0232399P.
2000US-0232398P.
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2000US-0234223P.
2000US-0234274P.
2000US-0234997P.
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2000US-0237038P.
2000US-0237039P.
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2000US-0241808P.
2000US-0241809P.
2000US-0241826P.
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2000US-0246474P.
2000US-0246475P.
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2000US-0235484P.
2000US-0235834P.
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2000US-0246528P
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06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
14-SEP-2000;
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29-58-2000;
29-58-2000;
02-0CT-2000;
02-0CT-2000;
02-0CT-2000;
13-0CT-2000;
13-0CT-2000;
20-0CT-2000;
20-0CT-2
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08-NOV-2000;
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08-NOV-2000;
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Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 20.0%; Score 44; DB 4; Length 41; Best Local Similarity 35.5%; Pred. No. 1.3e+02; Matches 11; Conservative 7; Mismatches 9; Indels
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17-NOV-2000; 2000US-0249207P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249218P.
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17-NOV-2000; 2000US-0249218P.
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17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-0259180P.
01-DEC-2000; 2000US-0251898P.
05-DEC-2000; 2000US-0251868P.
06-DEC-2000; 2000US-0251868P.
06-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251868P.
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N-PSDB; AAL02598.
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2000US-0249215P
 25-SEP-2000; 25-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 29-SEP-2000; 20-CT-2000; 20-CT-200
    chronic nephritis; blood-related disorder; thrombosis.
                                                                                                                                                   2000US-0179065P.
2000US-018662BP.
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2000US-0189874P.
2000US-0199076P.
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2000US-0216880P.
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2000US-0216880P.
2000US-0216890P.
2000US-0216890P.
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2000US - 0225213P.
2000US - 0225213P.
2000US - 0225214P.
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2000US - 022547P.
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2000US - 02268B.
2000US - 02218B2P.
2000US - 02218B2P.
2000US - 02218B2P.
2000US - 02218B2P.
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2000US-0229509P

2000US-0230431P

2000US-023143P

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2000US-0231244P

2000US-0231244P

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2000US-0231414P

2000US-0232391P

2000US-0232391P
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2000US-0234997P
                                                          WO200155316-A2
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18-APR-2000;
19-MAY-2000;
07-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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25-SEP-2000;
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                                 Homo sapiens
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Length 25; Indels

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Human ErbB2 peptide #3.
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                WPI; 2001-451929/48.
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                                                                                                     Query Match
Best Local Similarity
Matches 11; Conserv
                   N-PSDB; AAS40271
                                                                                                Sequence 41 AA;
                                                                                                                                                                                      JP2001218589-A.
                                                                                                                                                                                                          02-DEC-1999;
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                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                             14-AUG-2001
         Rosen CA,
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MEC (major histocompatibility complex) class II molecules on antigen-
presenting cells and are capable of activating epitope-specific CD4+
helper T cells. The invention also relates to a cell-mediated immunity
activation composition comprising an ErbB2 epitope peptide of the
invention, nucleic acids encoding a peptide of the invention, vectors and
ransformants comprising such nucleic acids, a method of determining the
number of CD4+ T cells reactive with ErbB2, and a method of preparing an
ErbB2 epitope peptide. The peptides of the invention are useful as immune
system activators and in the field of drug research. The present sequence
represents an ErbB2 peptide corresponding to residues 11-55 of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a fragment of the human ErbB2 extracellular domain corresponding to amino acids 22-53 which is capable of binding the monoclonal antibodies 7C2 and 7F3. This region is used in a method to identify antibodies which bind to ErbB2 and induce apoptosis of a cell which overexpresses ErbB2. The antibodies can also be used to detect ErbB2 on a cell. The antibodies can be used for treating disorders such as beingn or malignant tumours, (e.g. renal, liver, kidney, bladder, breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head and neck tumours), leukemia's and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic and other glandular, macrophagal, epithelial, stromal and blastocoelic disorders, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New anti-ErbB2 antibodies - which induce apoptosis in cells which overexpress ErbB2, used to treat e.g. tumours or inflammatory, anglogenic or immunologic disorders.
peptides of the invention, which are 15-25 amino acids in length, bind MHC (major histocomparibly two community)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ExbE2; epitope; monoclonal antibody; identification; apoptosis;
detection; treatment; disorder; tumour; benign; malignant; leukaemia;
lymphoid malignancy; inflammation; angiogenic; immunological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human ErbB2 extracellular domain protein fragment (aa 22-53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ñ
                                                                                                                                                                                                                                                                                                                                                                                                                Score 42.5; DB 4;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scheuermann RH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 45; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW59346 standard; protein; 32 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13 VPASPDTGLDPLTVRRHV 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 LPASPETHLOML --- RHL 19
                                                                                                                                                                                                                                                                                                                                                                                                                19.3%;
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55, v.,
Best Local 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC. (TEXA ) UNIV TEXAS SYSTEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-261493/23.
                                                                                                                                                                                                                                                                                                                                                             Sequence 25 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-APR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fendly BM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW59346;
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                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel isolated human prostate cancer antigen
polynucleotides (I) and polypeptides (II). (I) and (II) are useful for
preventing, treating or ameliorating a medical condition when
administered. (I). (II) and the antibody to (II) are useful for treating,
comministered. (I). (II) and the antibody to (II) are useful for treating,
comministered. (I). (II) and the antibody to (II) are useful for treating,
complities, and blood-related disorders related to the reproductive
complities; and blood-related disorders e.g. thrombosis. (II) can be used
for testing and detection e.g. as a chromosomal marker and in forensics.
(I) and the anti-(II) antibody can be used in testing and detection in
immunossays. AAU22702-AAU22913 represent the human prostate cancer
antigen amino acid sequence data for this patent did not form part of
invention. Note: The sequence data for this patent did not form part of
the printed specification, but was obtained in electronic format directly
committee of the printed process the printed process the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ErbB2; human; avian erythroblastic leukaemia viral oncogene homologue 2;
                                                                                                                                                                                                                   Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the reproductive system including prostate cancer and also for testing and detection e.g. diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel peptide useful in drug research has an immune activating ability.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44; DB 4; Length 41;
Pred. No. 1.3e+02;
7; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 KLRFLQTEDSWVPASPDTGLDPLTVR---RH 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunostimulation; CD4+ T cell activation.
                                                                                                                                                                                                                                                                                                                       Claim 11; SEQ ID NO 423; 546pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 5; 14pp; Japanese.
                                                                                            Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG66872 standard; peptide; 25
                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.0%;
35.5%;
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                                                                                         Barash SC,
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The invention relates to treating cancer in a human susceptible to or diagnosed with a disorder characterized by overexpression of ErbB2 creeptor. The method comprises administering an initial dose of at least approx.5 mg/Ks of the anti-ErbB2 antibody, and administering subsequent doses of the antibody in approximately the same amount or less than the initial dose. The method is useful for treating a disorder characterized initial dose. The method is useful for treating a disorder characterized by overexpression of ErbB2 receptor, particularly a benign or malignant tumour, or a cancer. The cancer is selected from breast cancer (particularly metastatic breast carcinoma), leukemia, squamous cell cancer, small-cell lung cancer, non-small cell lung cancer, pancreatic cancer, gastrointestinal cancer, non-small cell lung cancer, ovarian cancer, liver cancer, bladder cancer, hepstoma, colon cancer, ovarian cancer, inver cancer, bladder cancer, hepstoma, colon cancer, ovarian cancer, invercancer, vulval cancer, thyroid cancer, hepstic cancer, cancer, pastivary gland carcinoma, kidney cancer, cancer, prostete cancer, vulval cancer, thyroid cancer, hepstic cancer, cancer, pastivary gland carcinoma and various types of head encek cancer. The present sequence represents the 7C2/7F3 peptide epitope of ErbB2, recognised by MADS 7C2 and 7F3 as determined by deletion mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Treating a human patient with a disorder characterized by overexpression of ErbB2 receptor such as a tumor or cancer (e.g. metastatic breast carcinoma) comprises administering several dosages of an anti-ErbB2
                                                                                                                                                                                                                                          receptor; anti-ErbB2 antibody; tumour; cancer; breast cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.3%; Score 42.5; DB 4; Length 32; 55.6%; Pred. No. 1.6e+02; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                    leukemia, cytostatic, carcinoma, epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure, Page 64; 71pp; English.
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                                                     AAB62075 standard; peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-AUG-2000; 2000WO-US023391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0151018P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-JUN-2000; 2000US-0213822P
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14 LPASPETHLDML---RHL
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                                                                                                                                                                                           ErbB2 7C2/7f3 epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-235058/24.
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                                                                                                                                                                                                                                                                                                                                                          WO200115730-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-AUG-1999;
                                                                                                                                             29-MAY-2001
                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          08-MAR-2001
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                                                                                                   AAB62075;
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                                                                                                                                                                                                                                          ErbB2
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Matches
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       RESULT 12
                               AAB62075
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Domain; human; erbB2; receptor; antibody; overexpression; anthracycline; chemotherapeutic agent; tumour; cancer; breast; squamous cell; cervical; non-small-cell lung; gastrointestinal; parcreatic; glioblastoma; ovarian; liver; bladder; hepatcoma; colon; colorectal; endometrial carcinoma; ealivary gland; kidney; prostate; vulva; thyroid; hepatic carcinoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents the 7C2/7F3 epitope from domain 1 of the human erbB2 receptor protein. ErbB2 protein is used for raising antibodies for treating a human with a disorder characterised by overexpression of the ExbB2 receptor, using a combination of an anti-ErbB2 antibody and a chemotherapoutic agent other than an anthracycline derivative. Disorders characterised by overexpression of the ErbB2 receptor include benign or malignant tumours. The cancer may be breast, squamous cell, (non)-small liver, bladder, hepatoma, collon, colorectal, endometrial carcinoma, salivary gland carcinoma, kindey, prostate, vulval or thyroid cancer, hepatic carcinoma and various forms of head-and-neck cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New combination of an anti-ErbB2 antibody and a chemotherapeutic agent
                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                             3,
                                                                                               Length 32;
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                                                                                                                                          2; Indels
inflammatory, angiogenic and immunologic disorders
                                                                                          Score 42.5; DB 2;
Pred. No. 1.6e+02;
3; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human erbB2 receptor-derived epitope 7C2/7F3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 35; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                       AAY14575 standard; peptide; 32 AA.
                                                                                                                                          3;
                                                                                                                                                                                      13 VPASPDIGLDPLTVRRHV 30
                                                                                                                                                                                                                                  14 LPASPETHLDML---RHL 28
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14 LPASPETHLDML---RHL 28
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                                                                                            19.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 14-SEP-1999. (first entry)
                                                                                     Query Match
Best Local Similarity 55.6'
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 55.6
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        salivary gland; kidney
head-and-neck; epitope
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                                              Sequence 32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                      AAY14575;
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Homo

RESULT 11 AAY1457

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09-MAR-2001 (first entry)

Best Loca Matches

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Query Match
Best Local Similarity 55.00,
"...hes 10; Conservative
                                                          (GETH ) GENENTECH INC
                                                                     WPI; 2001-016161/02.
                                    WO200069460-A1.
                                                                                                                                              Sequence 32 AA;
                                                     14-MAY-1999;
                              Homo sapiens.
                                         23-NOV-2000
                                                                Cohen RL;
                                                                                                                                                                                        ADB84514;
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The invention relates to an isolated or purified nucleic acid from a virus associated with multiple sclerosis and/or rheumatoid arthritis, comultiple sclerosis associated virus (MSRV)-1. The nucleic acids comprise pol, gas or reverse transcriptase genes (or their fragments) encoding the proteins or defined peptides (including immunodominant peptides.

CC antignato peptides or conserved motifs). Also included are a process for antignant peptides or conserved motifs). Also included are a process for detecting a virus associated with multiple sclerosis or rheumatoid arthritis, a virus associated with multiple sclerosis or rheumatoid arthritis, a princer for the amplification by polymerisation of a nucleic acid of a viral material associated with multiple sclerosis or rheumatoid arthritis, a polypeptide exhibiting an inhibitory activity from MSRV, and an antibody directed against the MSRV-1 virus obtained by immunologically reacting a human or animal body or cells with an immunogenic agent consisting of the antigenic polypeptide defined above. The nucleic acids are useful for detecting a biological sample a virus associated with multiple sclerosis or rheumatoid arthritis, or for detecting in a biological sample, the presence of or exposure to a virus associated with multiple sclerosis or rheumatoid arthritis. The present of the patent do not match the SEQ ID numbers in the sequence. Note: The SEQ ID numbers for the sequences as displayed in the main body of the patent do not match the SEQ ID numbers in the sequence listing.

C sequences the authors intended to claim.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated or purified nucleic acid associated with multiple sclerosis and/or rheumatoid arthritis, useful for detecting a virus associated with multiple sclerosis or rheumatoid arthritis in a biological sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perron H, Besseme F, Bedin F, Paranhos-Baccala G;
Komurian-Pradel F, Jolivet-Reynaud C, Mandrand B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42; DB 7; Ler
Pred. No. 1.5e+02;
4; Mismatches 7;
reverse transcriptase; ribonuclease H; antigen.
                                                 Multiple sclerosis associated retrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19 TGLDPLTVRRHVPA-----VWVLLS 38
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                                                                                                                                                                                                             97US-00979847
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34.6%;
                                                                                                                                                                                                                                                                 96US-00756429
                                                                                                                                                                                                                                                                                                             PERRON H.
BESEME F.
BEDIN F.
PARAHGS-BACCALA G.
KOMURIAN-PRADEL F.
JOLIVET-REYNAUD C.
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GARSON J A.
TUKE P W.
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N-PSDB; ADB84553.
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                                                                                                  US2003039664-A1.
                                                                                                                                                                                                             26-NOV-1997;
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                                                                                                                                                         27-FEB-2003.
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(MAND/)
(GARS/)
(TUKE/)
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(KOMU/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel method of treating a human patient susceptible to or diagnosed with a tumour expressing the ErbB2 (HER2, cserb-B2) tumour antigen. The method comprises treating the patient with an expension of the musically, and then treating the patient with the anti-ErbB2 antibody or a chemocherapeutic agent. In the patient with the anti-ErbB2 antibody or a chemocherapeutic agent. In the patient with the anti-ErbB2 antibody 4D5, which binds to the an epitope on the extracellular domain of ErbB2 (residues 561-625; AAB48766). The method of the invention is used to treat a human patient susceptible to, or diagnosed with breast tumour, squamous cell tumour, small cell lung tumour, non-small cell lung tumour, gastrointestinal tumour, small cell lung tumour, colorctal tumour, glioblastoma, hepatoma, cervical tumour, ovarian tumour, or a tumour of the lung and or neck. The present sequence represents the epitope of the human ErbB2 (residues 22-58) which binds to the monoclonal antibodies of the account of the monoclonal antibodies of the account of the invention and in the coll of the monoclonal antibodies of the account of the monoclonal antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating a patient susceptible to, or diagnosed with, a tumor associated with breast, squamous cell, colon, kidney, liver by administering anti-ErbB2 antibody before and after surgical removal of the tumor.
                                                         Human ErbB2; HER2; c-ERb-B2; monoclonal antibody 7C2; 7F3; epitope; extracellular domain; humanised anti-ErbB2 antibody; antiproliferative; cancer; tumour; breast; squamous cell tumour; small cell lung tumour; non-Emall cell lung tumour; garrointestinal tumour; panoreatic tumour; colorectal tumour; glioblastcma; hepatoma; cervix; ovary; the liver; bladder; colon; colorectal; endometrium; vulva; salivary gland; kidney; prostate; head; neck; tumour antigen; anticancer.
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             Human ErbB2 7C2/7F3 epitope (residues 22-53).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MSRV-1B pol region isolate #3 protein #3.
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Tuke PW;

Garson JA,

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Gaps

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Length 27; Indels

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AAY98932 standard; peptide; 15 AA
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AAY98932;

07-AUG-2000 (first entry)

HLA class II binding antigen epitope peptide #121

Human leucocyte antigen; HLA class II; antigen epitope; pharmaceutical; immune response; chronic viral disease; cancer; autoimmune disease; rheumatoid arthritis; multiple sclerosis; myasthenia gravis; AIDS; allograft rejection; allergy; lyme disease; hepatitis; prostate cancer; glomerulonephritis; food hypersensitivity; malaria.

Unidentified

WO9961916-A1

02-DEC-1999.

28-MAY-1999; 99WO-US012066.

9-MAY-1998; 98US-0087193

(EPIM-) EPIMMUNE INC.

Sette A, Southwood S, Sidney J;

WPI; 2000-097143/08.

New compositions containing immunogenic peptide epitopes for various HLA class II DR molecules useful for inducing helper T cell response.

Claim 1; Page 42; 60pp; English.

The present invention relates to a new pharmaceutical composition comprising a unit dose form of a peptide, or analogue, comprising an epitope selected from those represented by peptides AAY98812-Y99339 which are derived from various antigens for various human leucocyte antigen class DR molecules, representative of the world winde population. The peptide hanalogue binds to an HLA class II molecule at an IC-50 of less than or equal to 1,000 nM. The pharmaceutical focuses the immune response the laper T cell response. The pharmaceutical focuses the immune response to the diseases and cancer. Examples of diseases that can be created using the peptide containing pharmaceutical include autoimmune treated using the peptide containing pharmaceutical include autoimmune created using the peptide containing pharmaceutical include autoimmune diseases (rheumatoid arthritis, multiple sclerosis, and myasthenia created using the peptide epitopes can be used to enhance immune response against other immunogens administered with the peptides. Or streptococcal endocarditis or glomenlonephritis and food hypersensitivities. The peptide epitopes can be used to enhance immune response against other immunogens administered with the peptides or Diseases which can be treated using immunogenic mixtures include prostate carcinoma, lymphoma, and condyloma acuminatum. The peptides may also be useful as diagnostic or therapeutic agents. The peptides may also be useful as diagnostic creargnorms, for example, to determine the susceptibility of an individuals will be at substantial fisk of developing chronic infection. Creargnorms will be at substantial fisk of developing chronic infection. The selection of appropriate T and B cell epitopes should allow the epitopes of pathogens which are characterized by high sequence epited by a period of pathogens which are characterized by high sequence.

Sequence 15 AA;

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Ouery Match
18.9%; Score 41.5; DB 3; Length 15;
Best Local Similarity 58.8%; Pred. No. 86;
Matches 10; Conservative 2; Mismatches 2; Indels 3; Gaps 1;
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53

13 VPASPDTGLDPLTVRRH

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January 26, 2005, 15:53:27; Search time 144 Seconds (without alignments) 102.867 Million cell updates/sec
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1 TKLRFLQTEDSWVPASPDTG......DPLTVRRHVPAVWVLLSRDP 41
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		sequence 29276, A	5286, Ap	423, App	213057,	2. Appli	2, Appli	334035,	249550,	3951, Ap				
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
	ΙD	US-10-029-386-29276	US-09-764-891-5286	US-10-091-572-423	US-10-424-599-213057	US-10-356-824-2	US-10-406-925-2	US-10-429-519-2	US-10-356-824-2	US-10-600-152-2	US-10-909-998-2	US-10-425-115-334035	US-10-425-115-249550	US-10-149-138-3951
	DB	14	10	14	15	14	14	14	15	15	17	17	17	15
	l Query Match Length DB	40	41	41	41	32	32	32	32	32.	32	37	40	15
ď	Query Match	22.0	20.0	20.0	19.5	19.3	19.3	19.3	19.3	19.3	19.3	19.1	19.1	18.9
	Score	48.5	44	44	43	42.5	42.5	42.5	42.5	42.5	42.5	42	42	41.5
	Result No.	1	7	ო	4	2	9	7	80	6	10	11	12	13

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88.6 88.6 88.6 88.6 88.6 88.6 88.7 88.2 88.3	-29276 No US20030194704A1 ORMATION: Rank, David R. Hanzel, David R. Hanzel, David R. HANZEL, DAVID R. NUENTION: ENCE: AEOMICA-X-2 ELICATION NUMBER: US LING DATE: 2001-12-2 SEQ ID NOS: 34288 AAHDOMAX SEQUENCE LIST 9276 HOMO SAPIENSED IONAMATION: EXPRESSED IONAM
222 22 22 22 22 22 22 22 22 22 22 22 22	RESULT 1 Sequence 29276, Application US/10029386 Publication No. US20030194704A1 GENERAL INFORMATION: APPLICANT: Penn, Sharron G. APPLICANT: Penn, Sharron G. APPLICANT: Penn, Sharron G. APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. TITLE OF INVENTION: HUMAN GENOME-DERIVED SI TITLE OF INVENTION: EXPRESSION ANALYSIS TW FILLE REPRESENCE: AECONICA-X-2 CURRENT APPLICATION UNBER: US/10/029,386 CURRENT APPLICATION UNBER: US/07/029,386 CURRENT PILING DATE: 2001-12-20 NUMBER OF SEQ ID NOS: 34288 SOFTWARE: Annomax Sequence Listing Engine v COTHER INFORMATION: EXPRESSED IN BONE MARRO OTHER INFORMATION: EXPRESSED IN HEART, SIG COTHER INFORMATION: SIGN COTHER INFORMATION
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PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/234, 274
PRIOR PRIOR APPLICATION NUMBER: 60/234, 274
PRIOR FILING DATE: 2000-09-27
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
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PRIOR PRIOR DATE: 2000-09-12
PRIOR PRIOR DATE: 2000-09-12
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PRIOR PLING DATE: 2000-10-20
PRIOR PLING DATE: 2000-09-13
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APPLICATION NUMBER: 60/241,787
FILING DATE: 2000-10-20
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APPLICATION NUMBER: 60/239,937
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                                                                                                                     Sequence 5286, Application US/09764891
FUBLICALION NO. US20030077808A1
GENERAL INFORMATION:
FILLS REPERENCE:
FULL REPERENCE:
CURRENT APPLICATION NUCLEIC Acids, Proteins, and Antibodies
FILLS REFERENCE:
CURRENT PILION DATE:
CURRENT APPLICATION NUMBER: US/09/764,891
FILLS REPERENCE:
FOLIO BATE:
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 5286
LENGTH: 41
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE SPERICATION NUMBER: US/10/091,572

CURRENT APPLICATION NUMBER: US/2-6/5

PRIOR APPLICATION NUMBER: 00/179,065

PRIOR PLICATION NUMBER: 60/129,065

PRIOR FILING DATE: 2000-01-11

PRIOR PLICATION NUMBER: 60/21/486

PRIOR PLICATION NUMBER: 60/21/487

PRIOR PLICATION NUMBER: 60/21/47

PRIOR PLICATION NUMBER: 60/21/47

PRIOR PLICATION NUMBER: 60/21/47

PRIOR PLICATION NUMBER: 60/225,57

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PRIOR PLICATION NUMBER: 60/225,267

PRIOR PLICATION NUMBER: 60/216,489

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PRIOR PLICATION NUMBER: 60/216,49
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PRIOR FILING DATE: 2000-08-14
PRIOR APPLICATION NUMBER: 60/251,869
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APPLICATION NUMBER: 60/246,532
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APPLICATION NUMBER: 60/215,135
FILING DATE: 2000-06-30
APPLICATION NUMBER: 60/225,266
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APPLICATION NUMBER: 60/232,401
                                                      APPLICATION NUMBER: 60/249,216
FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/249,210
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FILING DATE: 2000-08-22
APPLICATION NUMBER: 60/225,214
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FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/231,244
                                                                                                FILING DATE: 2000-11-17
APPLICATION NUMBER: 60/226,681
                                                                                                                                             LICATION NUMBER: 60/225,759
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/249,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICATION NUMBER: 60/249,212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LICATION NUMBER: 60/249,244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLICATION NUMBER: 60/249,211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLICATION NUMBER: 60/249,264
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                           PRIOR
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEC ID NOS: 285684
SEC ID NO 213057
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; Sequence 2, Application US/10356824
; Publication No. US20030147884A1
; GENERAL INFORMATION:
; APPLICANT: Bak, Steve
; APPLICANT: Baton, Virginia
; TITLE REFERENCE: P1256R1
; CURRENT APPLICATION: TREATMENT WITH ANTI-ErbB2 ANTIBODIES
; FILE REFERENCE: 10256.824
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/10/356,824
; CRRENT FILING DATE: 1998-12-10
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/069,346
; RIOR APPLICATION NUMBER: EARLIER FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 9
; SEQ ID NO 2
; LENGTH: 32
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US-10-424-599-213057
                                                                                                                                                                                                                                                                                                                                                                                                                                   2 KLRFLQTEDSWVPASPDTGLDPLTVR---RH 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 213057, Application US/10424599; Publication No. US20040031072A1; GENERAL INFORMATION:
                                                                                      R FILING DATE: 2000-10-20
R APPLICATION NUMBER: 60/241,786
R FILING JOATE: 2000-10-20
R R APPLICATION NUMBER: 60/241,221
R APPLICATION NUMBER: 60/246,475
RR APPLICATION NUMBER: 60/246,475
RR PILING DATE: 2000-11-08
R FILING DATE: 2000-13-08
R RILING DATE: 2000-13-08
R RILING DATE: 2000-13-08
FILING DATE: 2000-09-14
APPLICATION NUMBER: 60/241,808
APPLICATION DATE: 2000-10-20
APPLICATION NUMBER: 60/241,826
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Best Local Similarity 46.27
....nea 12; Conservative
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ORGANISM: Glycine max
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Matches
  PRIOR
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Sequence 2, Application US/10600152
| Publication No. US20040037824A1
| GENERAL INFORMATION:
| APPLICANT: Baughman, Sharon A. |
| APPLICANT: Shak Steven | TILE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies | FILE REFERENCE: P1775A1 |
| CURRENT PILING DATE: 2003-06-20 | PRIOR PILING DATE: 2000-08-25 | PRIOR PILING DATE: 2000-08-25 | PRIOR PILING DATE: 1999-08-27 | PRIOR PILING DATE: 1990-08-27 | PRIOR PILING DATE: 1900-06-23 | PRIOR PILING DATE: 2000-06-23 | PRIOR PILING DATE: 2000-06-23 | PRIOR PILING DATE: 3000-06-23 | PRIOR PILING DATE: 3000-06-23 | PRIOR PILING DATE: 3000-06-23 | PRIOR PILING DATE: 3000-06-35 |
                                                                           Sequence 2, Application US/10356824

Publication No. US20040037823A9

GENERAL INFORMATION:
APPLICANT: Boak, Steve
APPLICANT: Paton, Virginia
ITLE OF INVENTION: TREATMENT WITH ANTI-ErbB2 ANTIBODIES
FILE REFERENCE: P1256R1
CURRENT APPLICATION NUMBER: US/10/356,824
CURRENT APPLICATION NUMBER: US/09/208,649
PRIOR PILING DATE: 1998-12-10
PRIOR PLING DATE: L1989-12-10
PRIOR PLING DATE: EARLIER APPLICATION NUMBER: US 60/069,346
PRIOR PLING DATE: EARLIER PILING DATE: 1997-12-12

SEQ ID NOS: 9
SEQ ID NOS: 9
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Pred. No. 2.7e+02;
3; Mismatches 2;
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Pred. No. 2.7e+02;
3; Mismatches 2;
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14 LPASPETHLDML---RHL 28
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55.6%;
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Best Local Similarity 55.00,
-hog 10; Conservative
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Best Local Similarity 55.67
Matches 10; Conservative
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ORGANISM: Homo sapiens
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US-10-600-152-2
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US-10-909-998-2
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Fublication No. US20030170234A1
GENERAL INFORMATION:
APPLICANT: Shak, Steve
APPLICANT: Paton, Virginia
TITLE OF INVENTION: TREATMENT WITH ANTI-ExbEZ ANTIBODIES
CURRENT APPLICATION UNDHER: US/10/406,925
CURRENT APPLICATION NUMBER: US/09/209,023
PRIOR APPLICATION NUMBER: US/09/209,023
PRIOR PILING DATE: 1998-12-1
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/209,023
PRIOR FILING DATE: BALLIER PILING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 9
                                                                                                                                                                           Gaps
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                                                                                                            Length 32;
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19.3%; Score 42.5; DB 14; Length 32;
Best Local Similarity 55.6%; Pred. No. 2.7e+02;
Matches 10; Conservative 3; Mismatches 2; Indels
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TITLE OF INVENTION: TREATMENT WITH ANTI-ErbB2 ANTIBODIES
TITLE REFERENCE: P1757R1
FILE REFERENCE: P1757R1
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US/09/568,322
PRIOR APPLICATION NUMBER: US/09/568,322
PRIOR PLILING DATE: 2000-05-09
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 4
SEQ ID NOS: 4
                                                                                                                                                                    Indels
                                                                                         Query Match 19.3%; Score 42.5; DB 14; Best Local Similarity 55.6%; Pred. No. 2.78+02; Matches 10; Conservative 3; Mismatches 2;
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Publication No. US20030170235A1
GENERAL INFORMATION:
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14 LPASPETHLDML---RHL 28
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14 LPASPETHLDML---RHL 28
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14 LPASPETHLDML---RHL 28
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; ORGANISM: Homo sapiens US-10-356-824-2
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US-10-406-925-2
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Best Local Similarity
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Gaps

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Length 32;

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Indels
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Publication No. US2005002928A1
GENERAL INFORMATION:
APPLICANT: Paton, Virginia
TITLE OF INVENTION: TREATMENT WITH ANTI-ErbB2 ANTIBODIES
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Length 32;

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APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Suthwood, Scott
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cestis, Esteban
APPLICANT: Keogh, Elisa
TITLE OF INVENTION: HERZ/neu Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: HERZ/neu Using Peptide and Nucleic Acid Compositions
TITLE OF INVENTION: HERZ/neu Using Peptide
FILE REPERBUE: 2000-014001
CURRENT APPLICATION NUMBER: US/10/149,138
CURRENT FILING DATE: 2000-06-10
FRIOR PELING DATE: 1099-12-11
FRIOR PELING DATE: 1099-12-11
FRIOR FILING DATE: 1099-12-11
SRIOR PELING DATE: 1099-12-11
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CURRENT APPLICATION NUMBER: US/10/149,138
PRIOR APPLICATION NUMBER: PCT/USO0/33591
PRIOR APPLICATION NUMBER: PCT/USO0/33591
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                                                                                                                                           Query Match
Best Local Similarity 36.4%; Pred. No. 4e+02;
Matches 8; Conservative 5; Mismatches 7; Indels
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; OTHER INFORMATION: Artificially Synthesized Peptide
US-10-149-138-3951
                                ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_159174C.1.pep
US-10-425-115-249550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 41.5; DB 15;
Pred. No. 1.5e+02;
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Best Local Similarity 58.8%; Pred. No. 1.5e
Matches 10; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 3951, Application US/10149138; Publication No. US20040018971A1; GENERAL INFORMATION:
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; Publication No. US20040018971A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                            9 EDSWVPASPDTGLDPLTVRRHV 30
                                                                                                                                                                                                                                                                                            6 QETWM--DPAIGLTPYDVHKHV 25
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fikes, John
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
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APPLICANT: Southwood, Scott
APPLICANT: Chemut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Keogh, Elissa
     ORGANISM: Zea mays
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Ea Royalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Chou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT APPLICATION NUMBER: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Move Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NO 334035
LENGTH: 37
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19.1%; Score 42; DB 17; Length 37;
Best Local Similarity 53.8%; Pred. No. 3.6e+02;
Matches 7; Conservative 3; Mismatches 3; Indels
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US-10-425-115-334035
                    CURRENT APPLICATION NUMBER: US/10/909,998
CURRENT FILING DATE: 2004-00-02
PRIOR APPLICATION NUMBER: US/09/209,023
FRIOR FILING DATE: 1998-12-10
PRIOR PLICATION NUMBER: US 60/069,346
FRIOR PLING DATE: 1997-12-12
NUMBER OF SEQ ID NOS: 9
SEQ ID NOS: 9
LENGTH: 32
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Publication No. US20040214272A1
GENERAL INFORMATION:
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14 LPASPETHLDML---RHL 28
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Best Local Similarity 55.65
Matches 10; Conservative
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; ORGANISM: Homo sapiens
US-10-909-998-2
FILE REFERENCE: P1256R3
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WESULT 15
US-10-149-138-3951

is Sequence 3951, Application US/10149138

is Deducate 3951, Application US/10149138

is General 3951, Application US/10149138

is GENERAL INPORMATION:

is APPLICANT: Fikes, John

is APPLICANT: Sette, Alessandro

APPLICANT: Sette, Alessandro

APPLICANT: Cells, Esteban

is APPLICANT: Cells, Esteban

is APPLICANT: Cells, Esteban

is APPLICANT: Robert

APPLICANT: Mobert

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is APPLICANT: Robert

is APPLICANT: Robert

is APPLICANT: Robert

is PRIOR ILING DATE: 2000.014001

is CURRENT FILING DATE: 2000-012-11

is PRIOR FILING DATE: 1999-12-11

is PRIOR FILING DATE: 1999-12-11

is SEQ ID NO 3951

is LENGTH: 15

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18.9%; Score 41.5; DB 15; Length 15;
Best Local Similarity 58.8%; Pred. No. 1.5e+02;
Matches 10; Conservative 2; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.9%; Score 41.5; DB 16;
58.8%; Pred. No. 1.5e+02;
tive 2; Mismatches. 2;
PRIOR APPLICATION NUMBER: US 09/458,299
PRIOR FILING DATE: 1999-12-11
NUMBER OF SEQ ID NOS: 4641
SOFTWARE PatentIn version 3.1
SEQ ID NO 4508
LENGTH: 15
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CTHER INFORMATION: Artificial Peptide

US-10-149-138-4508
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ORGANISM: Artificial Sequence
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Best Local Similarity 58.8%
Matches 10; Conservative
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Search completed: January 26, 2005, 16:05:52 Job time : 145 secs ٠,٠

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Sequence 56614, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 41398, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PATENTI Ver. 2.0
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US-09-430-323-26
US-09-402-181B-216
US-09-177-249-256
US-08-34-616-26
US-08-384-616-26
US-08-384-616-26
US-08-384-616-26
US-08-384-616-26
US-08-31-26-36
US-08-31-30-30
US-08-471-939-70
US-08-471-939-70
US-08-471-939-70
US-08-471-939-70
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; Pred. No. 19;
4; Mismatches
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; ORGANISM: Drosophila melanogaster
US-09-270-767-56614
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1 Similarity 36.4%;
12; Conservative
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Best Local Similarity 36.4
Matches 12; Conservative
    Query Match
Best Local Similarity
    US-09-270-767-41398
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    TYPE: PRT
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                                                                                                                                                     January 26, 2005, 15:47:17 ; Search time 38 Seconds (without alignments) 71.554 Million cell updates/sec
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1 TKLRFLQTEDSWVPASPDTG......DPLTVRRHVPAVWVLLSRDP
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

(cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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(cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                       GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-974-549A-216
US-08-854-050-26
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Listing first 45 summaries
                                                                                                               protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 41
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Pred. No. 46;
1; Mismatches 6; Indels
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APPLICANT: Ruben et al.
TITLE OF INVENTION: 29 Human Secreted Proteins
FILE REFERENCE: P2015P1
CURRENT APPLICATION NUMBER: US/09/257,179
CURRENT FILING DATE: 1999-02-25
GERLIER APPLICATION NUMBER: PCT/US98/17709
EARLIER FILING DATE: 1997-08-29
EARLIER APPLICATION NUMBER: 60/056,270
EARLIER APPLICATION NUMBER: 60/056,270
EARLIER APPLICATION NUMBER: 60/056,271
EARLIER APPLICATION NUMBER: 60/056,271
EARLIER APPLICATION NUMBER: 60/056,271
EARLIER FILING DATE: 1997-08-29
EARLIER PILING DATE: 1097-08-29
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Pred. No. 38;
3; Mismatches
                  Mismatches
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Patent No. 6410709
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14 LPASPETHLDML---RHL 28
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illarity 53.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 55.6*
                                                               27 RRHVPAVWVLLS 38
               7; Conservative
                                                                                                  6 RSYLPAIWLLLS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
US-09-257-179-96
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Best Local Similarity
                                                                                                                                                                                                                   US-09-648-067A-2
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US-09-257-179-96
               Matches
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APPLICANT: CHASSIN, Dorine
APPLICANT: CHASSIN, Dorine
APPLICANT: BELLET, Dominique
TITLE OF INVENTION: NEW PROFERIN CALLED EPIL/PLACENTIN, PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THIS PROTEIN AND PHARMACEUTICAL
TITLE OF INVENTION: PROPESITION CONTAINING SUCH, DNA CODING FOR SAID
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
TITLE OF INVENTION: PROTEIN
FILE REPERENCE: 017753-127
CURRENT PELLING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 09/174,465
PRIOR PILING DATE: 1998-10-19
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                      APPLICANT: COMMAN, Ahment
APPLICANT: CHASSIN, Dorine
APPLICANT: CHASSIN, Dorine
APPLICANT: CHASSIN, Dorine
APPLICANT: CHASSIN, Dorine
APPLICANT: BELLET, Dominique
TITLE OF INVENTION: NEW PROTEIN CALLED EPIL/PLACENTIN, PROCESS FOR THE
TITLE OF INVENTION: PREPARATION OF THIS PROTEIN AND PHARMACEUTICAL
TITLE OF INVENTION: PROTEIN
FILE REFERENCE: 017753-103
CURRENT PAPLICATION NUMBER: US/09/174,465D
CURRENT FILING DATE: 1998-10-19
PRIOR APPLICATION NUMBER: US 08/482,842
NUMBER: OS SEQ ID NOS: 16
SOFTWARE: PATENTIN OF THE OS SECONDOS: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Unknown Organism: EPIL - Early
; OTHER INFORMATION: Placenta Insulin-Like Peptide
US-09-174-465D-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of Unknown Organism:EPIL - Early CHER INFORMATION: Placenta Insulin-Like Peptide US-09-594A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.5%; Score 45; DB 3; Length 17; Best Local Similarity 58.3%; Pred. No. 7.8; Matches 7; Conservative 4; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45; DB 3; Length 17;
Pred. No. 7.8;
10 DSTWAPSIYTTG-SPLRDRR--PLIWDLSPTTP 39
                                                                                                                         US-09-174-465D-6

Sequence 6, Application US/09174465D

Patent No. 6180364

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09599564A Patent No. 6362318 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 RSYLPAIWLLLS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27 RRHVPAVWVLLS 38
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-599-564A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 6
LENGTH: 17
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1,

Gaps

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APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Lingner, Joachim
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Greeg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.2%; Score 40; DB 3; Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION NUMBER: US/08/974,549A
FILING APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
FILING DATE: 18-APR-1997
FILING DATE: 18-APR-1997
FILING DATE: 25-APR-1997
PRIOR APPLICATION NUMBER: US 08/846,017
PRIOR APPLICATION NUMBER: US 08/851,843
FILING DATE: 12-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
FRICK APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 14-AUG-1997
FRICK APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 14-AUG-1997
FRILNG DATE: 14-AUG-1997
FRIENG DATE: 14-AUG-1997
FRIENG DATE: 14-AUG-1997
FREERBUNCE/DOCKET NUMBER: 05-60000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: 2 SEQUENCE CHARACTERISTICS: LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-974-549A-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRIES COUNTRIES STATEMENT OF STATEMENT O
                                                                                                                                                                                                                                                                   APPLICANT: Cech, Thomas R.
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6093809el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Emparcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REERERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 06-MAY-1997
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NATA:
APPLICATION NUMBER: US 08/846,017
CLASSIFICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
CLASSIFICATION:
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US-08-974-549A-217
Sequence 217, Application US/08974549A
; Patent No. 6166178
                                                                                                                                                Sequence 27, Application US/08851843A Patent No. 6093809 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 RFLOT----EDSWVPAS 16
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18 RFLRTTAEKNDGWVPIS 34
                                                                                                              US-08-851-843A-27
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18 RFLRTTAEKNDGWVPIS
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Best Local Similarity 52.9%; Pred. No. 1.1e+02;
Matches 9; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 38;
                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Capman, Karen B.
APPLICANT: Chapman, Karen B.
APPLICANT: Andrews, William H.
ITILE OF INVENTION: No. 6261836el Telomerase
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Frantisco
STREET: Two Embarcadero Center, 8th Floor
COUNTRY: United States of America
COUNTRY: The Perlopy disk
COMPUTER READABLE FORM:
MEDIOM TYPE: Plocypy disk
COMPUTER READABLE FORM:
MEDIOM TYPE: Plocypy disk
COMPUTER READABLE FORM:
MEDIOM TYPE: Plocypy disk
COMPUTER: Determin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US 08/851,843
FILING DATE: 09-MAY-1997
CLASSIFICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
CLASSIFICATION S36
FRIOR APPLICATION S36
FRIUNG DATE: 10-OCT-1996
CLASSIFICATION S36
FRIUNG APPLICATION S36
FRIUNG APPLICAT
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18.2%; Score 40; DB 3; Le
Best Local Similarity 52.9%; Pred. No. 1.1e+02;
Matches 9; Conservative 1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                             Sequence 27, Application US/08854050 Patent No. 6261836
                                                                                                                                     |||:|
18 RFLRTTAEKNDGWVPIS 34
                                                                                                4 RFLOT----EDSWVPAS 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: not relevan
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STRANDEDNESS: no
                                                                                                                                                                                                                                                              RESULT 9
US-08-854-050-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
                                                                                                                                                                                        Harley, Calvin
Andrews, William H.
TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Twomsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002930US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
18.2%; Score 40; DB 3; 1
Best Local Similarity 52.9%; Pred. No. 1.1e+02;
Matches 9; Conservative 1; Mismatches 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vex
CURRENT APPLICATION DATA:
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATE:

APPLICATION NUMBER: US 08/654,050

FLING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/44,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/44,419

FILING DATE: 01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                              STATE: California
COUNTRY: United States of America
ZIP: 94111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: not relevant

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-430-323-27
| Sequence 27, Application US/09430323
| Patent No. 6309867
| GENERAL INFORMATION:
| APPLICANT: Cech, Thomas R. Lingner, Joachim
| Nakamura, Toru Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION
                                                                                                                                                                    Morin, Gregg B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 RFLOT----EDSWVPAS 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (415)
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Harley, Calvin B.
Andrews, William H.
TILE OF INVENTION: Human Telomerase Catalytic Subunit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/974,549A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-NOV-1997
PELLING DATE: 01-O7-1996
FILING DATE: 01-O7-1996
APPLICATION NUMBER: US 08/844,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/854,050 FILING DATE: 09-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 22-No. 6617110-2000 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 217:
US-09-721-456-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
                                                                        Sequence 217, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: <Unknown>
                                                                                                                                                                    Lingner, Joachim
                                                                                                                                                                                                                     Karen B
                                                                                                                                            APPLICANT: Cech, Thomas R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (415)
TELEFAX: (415) 57
N FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                     Chapman,
                                    US-09-721-456-217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION
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                                                                                                                                                                                 Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1e+02;
3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 38;
                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 9411-384
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: TSM PC compatible
SPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 015389-002620US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 40; DB 4;
Pred. No. 1.1e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
FILING DATE: 25-APR-1997
FILING DATE: 06-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,181B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/854,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/912,951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 217:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Ausenhus, Scott L. REGISTRATION NUMBER: 42,271
                     Sequence 217, Application US/09402181B Patent No. 6610839 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-AUG-1997
                                                                                APPLICANT: Cech, Thomas R.
Lingmer, Joachim
Nakamura, Toru
Chapman, Karen B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.2%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                 STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 9; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ
-402-181B-217
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Score 38.5; DB 1; Length 28;
Pred. No. 1.2e+02;
4; Mismatches 7; Indels
                                                                                                                                                                                                                         Score 39; DB 4; Length 38;
Pred. No. 1.5e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/596,081A
FLING DATE: 19901011
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 266983/1989
FILING DATE: 13-OCT-1989
ATTONEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 14, Application US/07596081A

Sequence 14, Application US/07596081A

Farent No. 5194586

GENERAL INFORMATION:
APPLICANT: Washittani, Yukiko
APPLICANT: Washittani, Yukiko
APPLICANT: Wanada, Kyoko
APPLICANT: Yamada, Kyoko
APPLICANT: Oka, Kiichiro
APPLICANT: Oka, Kiichiro
APPLICANT: Oka, Kiichiro
TITLE OF INVENTION: Peptides and Use Thereof
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Eric S. Spector
STREET: P.O. Box 2266 Eads Station
STREET: Vo. Box 2266 Eads Station
STREET: Virginia
COUNTRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KLRFLQTEDSWVPAS-----PDTGLD 22
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; ORGANISM: Drosophila melanogaster
US-09-270-767-56715
              CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 56715
LENGTH: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Spector, Eric S. REGISTRATION NUMBER: 22495
REFERENCE/DOCKET NUMBER: 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-415-1500
                                                                                                                                                                                                                      17.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.5%;
38.5%;
                                                                                                                                                                                                               Query Match
Best Local Similarity 62.5
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 38.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 703-415-1508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                               12 WVPASPDT 19
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11 WIPETPDT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-07-596-081A-14
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US-09-270-767-56715
Sequence 56715, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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         Pred. No. 1.1e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 2; Length 35;
Pred. No. 1.3e+02;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WordPerfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,306A

FILING DATE: 02-Oct-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 95/20080.4

FILING DATE: 02-Oct-1995

PRIOR APPLICATION NUMBER: 38/009,832

FILING DATE: 01-Jan-1996

ATTORNEY/AGENT INFORMATION:

NAME: Williams, Ph.D., Kathleen M.

REGISTRATION NUMBER: 34,380

REFERENCE/DOCKET NUMBER: 34,380

REGISTRATION INFORMATION:

NAME: Williams, Ph.D., Kathleen M.

REGISTRATION INFORMATION:

TELEFENCE (617) 345-910

TELEFAX: (617) 345-911

INFORMATION CE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

INFORMATION CE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    Sequence 39, Application US/08726306A
Patent No. 5958684
GENERAL INFORMATION:
APPLICANT: Van Leeuwen, Frederik Willem
APPLICANT: Burbach, Johannes Peter Henri
APPLICANT: Broselow: Diagnosis METHOD AND REAGENTS
NUMBER OF SEQUENCES: 189
CORRESSED: Banner & Witcoff, Ltd.
STREET: 1 Financial Center
STREET: WA
COUNTRY: US
ZIPT: MA
Best Local Similarity 52.9%; Pr
Matches 9; Conservative 1;
                                                                        4 RFLQT----EDSWVPAS 16
                                                                                                  17.7%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TKLRFLQTEDSWVP 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 35 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                   RESULT 13
US-08-726-306A-39
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Search completed: January 26, 2005, 16:02:48 Job time : 46 secs

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AL009365 H. sapiens
BVL7772 Sagm6347
222256 H. sapiens
AB035828 Coturnix
CQ080407 Sequence
CQ114259 Sequence
CQ153138 Sequence
CQ153138 Sequence
CQ274027 Sequence
CQ274027 Sequence
CQ274027 Sequence
CQ11266 Sequence
CQ1563 Sequence
CQ1563 Sequence
CQ1563 Sequence
CQ156439 Sequence
CQ156439 Sequence
CQ156439 Sequence
CQ154439 Sequence
CQ275317 Sequence
CQ2749156 Sequence
CQ274915 Sequence
CQ2749156 Sequence
CQ2749156 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BV165390 166 bp DNA linear STS 02-AUG-2004
M8U65-12 PCR fragment of the molecular marker, M8U63-Vr-TC1966
Vigna radiata STS genomic, sequence tagged site.
BV165390
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Pevelopment of Nuclear gene-derived Molecular Phylogenetic Markers
Linked to Legume Genetic Maps
Umpublished (2004)
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94 degrees C for 20 seconds
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MJ Research, Tetrad
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
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BV165391 M8U63-13
AF135376 Semibalan
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CAES Genomics Facility
University of California-Davis, Plant Pathology
One Shields Ave Davis, CA 95616, USA
Tel: 530 754 6501
Fax: 530 754 6617
Fax: 530 754 6617
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each 0.5 uM
each 250 uM
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Polymerization:
PCR Cycles:
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C0086407
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C0236438
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dNTP:
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VERSION
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DEFINITION
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AUTHORS
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BV200943 sgmm20546
AJ506605 Homo sapi
CQ660987 Sequence
Z26745 M.musculus
L35014 Mouse N.met
CQ679231 Sequence
CQ443803 Sequence
AJ20371 Homo sapi
CQ734281 Sequence
AX798801 Sequence
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Z55291 H.sapiens C
BD227006 Compounds
AR225406 Sequence
AK321476 Sequence
S68587 platelet-ty
S68588 platelet-ty
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                                                                                                                                    January 31, 2005, 18:09:35 ; Search time 1821 Seconds (without alignments) 7089.560 Million cell updates/sec
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                                                                                                                                                                                                                                                                      ...ccaagctacgtttccttcag 273
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                                                                                                                                                                                                                                                                                                                                                                                                                   3273528
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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HSA506605
CQ660987
MMSTS122
MUSNR2C01
CQ443803
HSA230371
CQ734281
AX798801
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273
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                                                                                                 - nucleic search, using sw model
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Maximum DB seq length: 273
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Perfect score:
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sqnm205467 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72 TACCCTTGAGAIGCGGGTCCGAGAIGGCAGCAAATTCGCAACCTGCTGGGGITGGCTCT 131
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I (bases 1 to 201)
Nelson, R. M. Marnellos, G., Kammerer, S., Hoyal, C.R., Shi, M.M., Cantor, C.R. and Braun, A.
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
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                                                                                                                                                                                                                                                                                                                                      Length 133;
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10.5%; Score 28.8; DB 4; Length 1.
Best Local Similarity 54.8%; Pred. No. 1.9e+03;
Matches 57; Conservative 0; Mismatches 47; Indels
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3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18522029018
Fax: 18582029020
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Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 201.
                                                                                             1. .133
/gene="DRD4"
/note="dopamine receptor D4"
/number=2
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Pharmaceuticals division
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BV200943.1 GI:48169634
                1. .133
/gene="DRD4"
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Canis familiaris DRD4 gene, intron 2, complete sequence, isolate:Q.
AB126591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="PCR-amplified genomic fragment using cross-species gene-specific primer sets"
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Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
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Novel Polymorphism of the canine dopamine receptor D4 gene intron
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/note="Light harvesting chlorophyll a/b-binding (CAB)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:157791"
/sex="Hermaphrodite"
/tissue_type="Leaf"
/clone_lib="PCK fragment of the molecular marker,
MsU63-Vr-TC1966"
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                                                                                                                                                                                                                                                                                                                      l. .166
/organism≂"Vigna radiata"
                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/cultivar="TC1966"
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Nehla, M., Luno, K., Schorpp, M., Pfeifer, D., Krause, S., Matyaiak-Scholze, U., Dierbach, H. and Boehm, T.
YAC/PI contigs defining the location of 56 microsatellite markers and several genes across a 3.4-cM interval on mouse chromosome 11 Mamm. Genome 6 (5), 321-331 (1995)
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                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (03-AUG-1994) Thomas Boehm, Dept. of Medicine I,
Molecular Medicine Group, Hugstetter Str. 55, Freiburg, 79106,
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                                                                                                                                                                                                                                                                                                                                                         10.4%; Score 28.4; DB 6; Length 262; 58.1%; Pred. No. 2.5e+03; tive 0; Mismatches 36; Indels
                                                                                                                                    Liew,C.C., Marshall,W.E. and Zhang,H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737A, 5913 12-SEP-2002;
Chondrogene Inc. (CA)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.musculus (D11Bhm122) sequence tagged site DNA. 236745.1 GI:1041471
                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Organiam="Mus musculus"
(mol_type="genomic DNA"
/errain="C57B1/6"
/db_xref="taxon:10090"
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Mus musculus
CQ660987.1 GI:42133182
                                       Homo sapiens (human)
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3 (bases 1 to 273)
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Matches 50; Conservative
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                                                             Homo sapiens
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                      PRI 07-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (08-JUL-2002) Kurth J., Department of Internal Medicine
I, University of Cologne, Joseph-Stelzmannstr. 9, Cologne, 50931,
GERMANY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 AGAGTTGGAGTCAGAGAATCGGTCAGCGATCCCTGAGGGCCGGTCGGCATCGTCATGGAC 67
                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
    HARDOGOS 227 bp DNA linear PRI 07-APR-160m0 sapiens partial IGLV3 gene, out of frame rearrangement, isolate case 2, GCE 149.
AJ506605
AJ506605.1 GI:27650792
IGLV3 gene; immunoglobulin lambda light chain; variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rearranged
/note="EBER-positive cell, located in interfollicular
                                                                                                                                                                                                                                     Kurth,J., Hansmann,M.L., Rajewsky,K. and Kuppers,R.
Epstein-Barr virus-infected B cells expanding in germinal cente
Of infectious mononucleosis patients do not participate in the
germinal center reaction
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/db_xref="PSEUDO:CAD53530.1"
<1. .>227
/gene="IGLV3"
/pseudo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
/isolate="case 2, GCE 149"
/db xref="taxon:9606"
/cell_type="B-lymphocyte"
/tissue_type="tonsil"
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chain variable region"
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Kurth, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,>227
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CQ660987/c
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  HSA506605/c
                                     DEFINITION
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Homo sapiens BF2N3-L3-C11 gene for immunoglobulin lambda chain AJ230371
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                                                                                                                                                                                                                                                                           63 ACCICCIGAIACCCITGAGAIGCGGGICCGAGAIGCCAGCAAAAITCGCAACCIGCTGGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 CTCAGGTTCTGGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCG 230
                                                                                                                                                                                                                                                                                                                 153 ACTITCITGIAGGCITCANACGCCCGACCTTNAGGCCAGCAGGACCCACCATCCGCITTT 94
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Farner, N.L.
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Immunoglobulin; immunoglobulin lambda chain; immunoglobulin superfamily; joining region; variable region.
Homo sapiens (human)
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Human polymuclectides and polypeptides encoded thereby
Patent: WO 019523.4 9563 06-DEC-2001;
Curagen Corporation (US)
Location/Qualifiers
                                                                                                                                                                                                  Length 154;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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10.2%; Score 27.8; DB 6; Length 1:
1 Similarity 56.2%; Pred. No. 3.7e+03;
50; Conservative 0; Mismatches 39; Indels
            Patent: WO 02070737-A 24157 12-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            194 bp DN
Sequence 9563 from Patent WO0192523.
CQ443803
                                                                                          /organism="Homo sapiens"
/mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                         123 GTTGGCTCTGGTCGGTTGGAGGGCGGCA 151

    .194
    /organism="Homo sapiens"
    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

                                                                                                                                                                                                                                                                                                                                                                                 93 TCTTGTAGGCGGTGGGATGCCGTCA 65
                                   Chondrogene Inc. (CA)
Location/Qualifiers
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Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                   MUSNR2C01 273 bp DNA linear ROD 23-JAN-1995
Mouse N-methyl-D-aspartate receptor subunit NR2C (NMDA2C) gene,
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200 CTTGAGAGGCAGCTGCAAGGCGGCAGCTGTGGAAGGCAGCTGCCGCGGCGCTTGATCTCTAG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                              Suchanek, B., Seeburg, P.H. and Sprengel, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Original source text: Mus musculus (strain SV129) (tissue library: Stratagene Lambda FIX II) adult liver DNA. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90 CCGAGATGGCAGCAAAATTCGCAACCTGCTGGGGTTGGCTCTGGGTCGGTTGGAGGGGGG 149
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L35014.1 GI:602738
N-methyl-D-aspartate receptor subunit NR2C; NMDA receptor subunit
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/tissue_type="liver"
/dev_stage="adult"
/lissue_lib="Stratagene_Lambda_FIX_II"
/lissue_lib="Stratagene_Lambda_FIX_II"
/lissue="NWDA2C"
/loce="NWDA2C"
/transcriptional start sites at basepairs 11, 12, 29"
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10.3%; Score 28; DB 10; Length 273;
Best Local Similarity 56.5%; Pred. No. 3.3e+03;
Matches 52; Conservative 0; Mismatches 40; Indels
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Compositions and methods relating to osteoarthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CQ679231 154 bp DNA Sequence 24157 from Patent WO02070737. CQ679231 CQ679231.1 GI:42191392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 GAGACGGCCCCCCGGCCTCGGCGCGCAG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. Chem. 270 (1), 41-44 (1995)
95113860
                                                                   140 CCGGTATTATCTGACAGCTCTCGGCATGT 112
                                          136 CGGTTGGAGGCGGCAGTGCTCGGCATGT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="SV129"
                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
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RICG332A 160 bp DNA linear STS 23-MAR-2002 Oryza sativa (japonica cultivar-group) genomic DNA, G332A, sequence
                                                                                                            PAT 08-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 CTGCTGGGGTTGGCTCTGGGTCGGTTGGAGGGCGGCCAGTGCTCGCATGTAGTGTTCTCA 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             205 CTCCTTGGCCCAGGTGACGACCGAGTCGACGAGGTTGCCCATCATGAGGTTCTCGGT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 GGTTCTGGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STS; Genomic; RFLP; Rice.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnolitophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 GCCGGTGTTCGAGCAGCAGCTGCTGTTGGCCACCGAGCGGCGAGCAGCAGCCGCTGGTA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-NOV-1993) Yuzo Minobe, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305, Japan (E-mail:MINOBE@rtcs0.riken.go.jp, Tel:0298-38-7441,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 160)
Minobe, Y.
Nucleotide sequence of sequence tagged site from japonica rice
Nipponbare as an RFLP marker
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 59 GTTTTATGAGGGCTGCAGTCAATGCTGACATGTGTGCTGAAGTCTTCAATCAGCTG
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                                                                                                                                                                                                                                                                               Breves, R., Maurer, K.H., Eck, J., Lorenz, P. and Zinke, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 235;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Indels
                                                                                                             linear
                                                                                                                                                                                                                                                                                              New glycosyl hydrolases
Patent: WO 03054177-A 287 03-JUL-2003;
Henkel Kommanditgesellschaft auf Aktien (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 27.2; DB 6;
Pred. No. 5.6e+03;
0; Mismatches 68;
                                                                                                             DNA
                                                                                                            AX798801 235 bp DN
Sequence 287 from Patent WO03054177.
AX798801
                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="unassigned DNA"
/db_xref="taxon:32644"
/note="Metagenom"
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Submitted (18-Nov-1993) to DDBJ by:
Yuzo Minobe
                                                                                                                                                                                                                                                                                                                                                                                         /organism="unidentified"
                                                                                                                                                                 AX798801.1 GI:37604879
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1 Similarity 50.0%;
68; Conservative (
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2 (bases 1 to 160)
Minobe, Y.
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                        103 AAAATTCGCAACCTGCTGGGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCAT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 ATAGTCAGCCTCATCCCCGGCTTGGGCTCTGCTGATGGTCAGGGTGGCCGTGTTCCCCGA 142
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 4.9e+03;
0; Mismatches 76; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                                                                                                                                                                                                                           /cell_line="single B lymphocyte"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent: WO 02068579-A 20215 06-SEP-2002;
PE Corporation (NY) (US)
Location/Qualifiers
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    .99
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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                                                                                                                                                                                                 /mol type="genomic DNA"
/isolate="donor JW"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                   1. .240
/gene="BF2N3-L3-C11"
                                                                                                                                                                                                                                                                                                                                                                                                        /gene="BF2N3-L3-C11"
/note="3J/23/P"
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CQ734281.1 GI:42321535
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                    (bases 1 to 240)
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Best Local Similarity 49.09
Matches 73; Conservative
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Dept. Rice Genome Research Program

176 GTTCTGGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGG 231

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BD237006 264 bp DNA linear PAT 17-JUL-2003 Compounds for remedy and diagnosis of lung cancer and method for
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A61P11/00,A61P35/00,C07K14/47,C07K16/18,C07K19/00,C12N1/19, PC
      C12NS/10, C12P21/08, C12Q1/68, G01N33/53, G01N33/574, G01N33/577//
(C12N1/21, C12R1:19), C12N15/00, A61K37/02, C12N5/00 CC n =
                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases 1 to 264)
Reed, S.G., Lode 264)
Compounds for remedy and diagnosis of lung cancer and method for painty the same
Patent: JP 2002516659-A 7 11-JUN-2002;
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C12N15/09,A61K35/14,A61K38/00,A61K39/00,A61K39/39,A61K39/395,
                                                                    120 GGGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGTGTTCTCAG 175
                                                                                              182 GGCCCGGCCTGGAGGACCCGCTGGCTTCCGTAGCTAGAGTTCTCCG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 ddartggggdgdggggdgagarmgacrrraacrgccccacgrrnrcwaggaaagdarr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 9.9%; Score 27; DB 6; Length 264; Best Local Similarity 54.3%; Pred. No. 6.4e+03; Matches 51; Conservative 1; Mismatches 42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JAN-1998 US 09/015029, 28-JAN-1998 US AR-1998 US 09/040828, 18-MAR-1998 US 09 UL-1998 US 09/122192, 23-JUL-1998 US 09/219245, 09/21998 US 09/219245, TONY N FRUDAK STEVEN G REED, MICHAEL J LODES, TONY N FRUDAK
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focation/Qualifiers
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PF 26-JAN-1999 JP 2000529432
PF 28-JAN-1998 US 09/015029,
18-MAR-1998 US 09/040828,18-WI
23-JUL-1998 US 09/122192,23-JU
22-DEC-1998 US 09/219248
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JP 2002516659-A/7
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JP 2002516659-A/7.
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Homo sapiens
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BD237006
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BD237006
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I sapiens CpG island DNA genomic Msel fragment, clone 140c7,
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Dodsworth,S.J., Huckle,E., Wilkinson,P. and Micklem,G.
Dodsworth,S.J., Huckle,E., Wilkinson,P. and Micklem,G.
Direct Submission
Submitsed (16-0cr-1995) The Sanger Centre, Hinxton, Cambridgeshire,CB10 1RQ, England. B-mail contact: humquery@sanger.ac.uk
Vector: pGEM-5ZE(-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross, S.H., Charlton, J.A., Nan, X. and Bird, A.P. Purification of CpG islands using a methylated DNA binding column Nat. Genet. 6 (3), 236-244 (1994) 94282070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clones are available from the UK MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL: http://www.hgmp.mrc.ac.uk/ for details or contact: biohelp@hgmp.mrc.ac.uk.
Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:39947"
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9.9%; Score 27; DB 9; Length 241;
Best Local Similarity 51.7%; Pred. No. 6.46+03;
Matches 60; Conservative 0; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                        40; Indels
National Institute of Agrobiological Resources
                                                                                                                                                                                                                                                                                                             Score 27; DB 11;
Pred. No. 6.3e+03;
                                                                                                                                                                                                                                                                                              9.9%; Scor No. e.c. 56.0%; Pred. No. e.c. 0; Mismatches
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CGG island; genomic Msel fragment.
Homo sapiens (human)
Homo sapiens
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/clone_lib="CGI-1"
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                                                                                                                                                Location/Qualifiers
                                                          Japnan
Phone: 0298-38-7441
Fax: 0298-38-7468
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                                                                                                                                                                                                                                                                                                                                                      51; Conservative
                     Kannondai 2-1-2
Tsukuba, Ibaraki
                                                                                                                        PROJECT = 'RGP'
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Matches 51; Conserv
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235 CCAGGCCTGCACCAGCTCACGTACGTTTCC 268
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                                                                                                                                                        Search completed: January 31, 2005, 19:44:40 Job time : 1826 secs
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71

Gaps

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AA022458 ze70h07.r
AA032458 ze70h07.r
AA1348 mc86b02.r1
AA239107 mc96c09.r
AA239107 mc96c09.r
AA239107 mc96c09.r
AA239107 mc96c09.r
AA356051 v111e10.r
AA35609 H8938 MAR
BM066792 ie85a09.y
AV435800 AV43560
AV43580 AV435681
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AV434181 AV43181
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AV436270 AV43540
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BE774505 PM0-UMO01
                                                                January 31, 2005, 18:58:47 ; Search time 1938 Seconds (without alignments) 5133.151 Million cell updates/sec
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                                                                                                               US-10-057-813-13_COPY_1_273
273
1 atggagcactaccggaaagc......ccaagctacgtttccttcag 273
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                32822875 seqs, 18219865908 residues
                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                          OM nucleic - nucleic search, using sw model
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AA239107
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AA756051
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AW818811
AV430042
AV432681
AV434181
AV435325
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Maximum Match 100%
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CB885146 MA0060 HA BG93930 RC4-CT069 BE917539 RC4-CT069 BE717545 RC4-HT077 CNA53918 17000599 AV435417 AV435417 AV435026 AV435673 AV435026 AV435026 AL132127 FUBY AV435028 AV435028 BJ162793 BJ162793 AV435623 AV435623 AV435523 AV43563 AN435359 AV43595 AV435395 AV43595 AV508914 VC4606.11 CO698646 DG32-142C	ALIGNMENTS Minagz-i-16-0-UI ri UI-E-DM1 Homo Sapiens cDNA clone W1-agz-i-16-0-UI s', mRNA sequence. W1-agz-i-16-0-UI s', mRNA sequence. W1-agz-i-16-0-UI s', mRNA sequence. W1-agz-i-16-0-UI s', mRNA sequence. Dela Gi:19013017 Apiens (human) Dela Gia Metazaca; Chordata; Craniata; Vertebrata; Euteleostomi; des Iro 272) Dela Gia Metazaca; Chordata; Catarrhini; Hominidae; Homo. Dela Iro 272) Minagarian and subtraction: two approaches to facilitate gene ery Minagarian and subtraction: two approaches to facilitate gene ery Minagarian and subtraction: two approaches to facilitate gene ery Minagarian and subtraction: two approaches to facilitate gene ery Minagarian and subtraction: two approaches to facilitate gene ery Minagarian and subtraction: two approaches to facilitate gene ery Minagarian and subtraction: two approaches to facilitate gene ery Minagarian and subtraction: Dr. M. Bento Soares, Univeristy of Iowa sitherary preparation: Dr. M. Bento Soares, Univeristy of Iowa Distribution: Researchers may obtain clones from Research Minagarian erye manna; Minagarian erye manna; Minagarian erye manna; Minagarian erye wector: privi3-Pac (Pharmacia) with a modified polylinker; Site I: Rook Ri; Site 2: No Clone Iip- Minagarian erye wector: privi3-Pac (Pharmacia) with a modified polylinker; Site I: Rook Ri; Site 2: No Clone Iip- Minagarian erye wector: privial erye constructed efollowing tissue (s): lens. The library was constructed
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6:791-806, 1996. First strand CDNA syntheeis was primed with an oligo-dT primer containing a Not I site. Double stranded CDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT713-Pac vector. The oligonucleotide used to prime the synthesis of first-strand CDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CGATTAGGGA. This library was created for the program, Gene Discovery in the Visual System, supported by National Bye Institute (NEI)."
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ze70h07.rl Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone
MAM2E:364381 5', mRNA sequence.
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(base) to 26.

Hillier, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, M., Le, M., Chissoe, B., Morris, M., Parson, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.,
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according to Bonaldo, Lennon and Soares, Genome Research
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                        82.6%; Score 225.4; DB 4; Length 272; 99.1%; Pred. No. 1.5e-51; ive 0; Mismatches 2; Indels 0;
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Homo sapiens
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Matches 226; Conservative
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/organism="Homo sapiens" /mol_type="mRNA"

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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4306
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904-e. Vector identified by cross_march with the -minscore 20
pcr PRimers
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                           double-stranded CDNA was size selected, ligated to Eco KI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco KI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Katima Bonaldo. This library was constructed from the same fetus as the fetal lung library, Soares fetal lung NbHL19W."
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22213789
clone="IMAGE:364381"
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Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECORI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coll DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA alrand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coll Toplof' by electroporation method. The cDNA libraries constructed by this method are full-length enriched CDNA library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W48348 24-MAY-1996 mC86b02.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:355371 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCA 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/Mouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                   Score 135; DB 6; Length 220;
Pred. No. 1.4e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                          Query Match
49.5%; Score 135; UB
Best Local Similarity 100.0%; Pred. No. 1.4
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/organism="Mus musculus"
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Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:355371"
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Seq primer: mob.REGA+ET
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1 (bases 1 to 220)
1 (bases 2 to 220)
1 (bases 2 to 220)
2 (bh.K.J., Chu,M.Y., Kim,J.M., Park,H.S., Kim,S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CB117372 22-JAN-2003
K-EST0162559 L4SNU368 Homo sapiens CDNA clone L4SNU368-30-H04 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sall; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
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/cell_type="Polygonal"
/cell_line="NU0-368"
/lab_host="Toplop" "
/clone_lib="L4SNU368"
/note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI;
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Pred. No. 1.6e-27;
0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Xim YS
Contact: Xim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Roeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Fat: +82-42-860-4470
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21C Frontier Korean EST Project 2001
Unpublished (2002)
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="L4SNU368-30-H04"
                                                                                                                                  /mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="pl108"
/clone_lib="MARC'2PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: yongsung@mail.kribb.re.kr
Plate: 30 row: H column: 04
High quality sequence stop: 220.
Location/Qualifiers

    194
/organism="Sus scrofa"

      BACKWARD: GTTTTCCCAGTCACGACG
Plate: 32 row: M column: 15
Seq primer: ATTTAGGTGACACTATAG.
                                                                         Location/Qualifiers
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Homo sapiens
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CB117372
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Best Local Similarity
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CB117372
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AA239107 21.7 bp mRNA linear EST 03-MAR-1997 my36c09.rl Barstead mouse pooled organs MPLRB4 Mus musculus cDNA clone IMAGE:697936 5', mRNA sequence.
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:431496
Seg primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 169.
Location/Qualifiers
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Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 37.7%; Score 103; DB 1; Length 256; Best Local Similarity 81.7%; Pred. No. 9.9e-18; Matches 143; Conservative 0; Mismatches 30; Indels
                                                             /tissue_type="mammary gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1396086"
                                                                                 /dev_stage="4 weeks"
/lab_host="DH108"
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                                                                    AII83131 256 bp mRNA linear EST 08-OCT-1998 ub93g04.rl Soares mammary gland NbMMG Mus musculus cDNA clone IMAGE:1396086 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTACCICCIGATACCCTIGAGAIGCGGGICCGAGAIGGCAGCAAAAIICGCAACCIGCIG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL , contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gapa
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The WashU-HIMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HIMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 43.0%; Score 117.4; DB 7; Length 251; Best Local Similarity 82.1%; Pred. No. 1e-21; Matches 147; Conservative 0; Mismatches 31; Indels 1;
        /tissue_type="embryo"
/dev.stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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High quality sequence stop: 252.
Location/Qualifiers
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
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AI183131
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AA756051.1 GI:2803249
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Best Local Similarity
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AA756051
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                                                                                  / Lissue type="pooled organs"
//dev stage="7 day"
//dev stage="7 day="7 d
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mb49d03.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone
IMAGE:332741 5', mRNA sequence.
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1 (Bases 1 to 246)
Marra, M.; Hillier, L.; Allen, M.; Bowles, M.; Dietrich, N.; Dubuque, T.;
Geisel, S.; Kucaba, T.; Lacy, M.; Le, M.; Martin, J.; Morris, M.;
Schellenberg, K.; Steptoe, M.; Tan, F.; Underwood, K.; Moore, B.;
Mateston, B.; Wylie, T.; Lennon, G.; Soares, B.; Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 ATGGAACAGTACCGG-AGGCCGGCTCTGTAGAGCTTCCAGCCTCATCACCAATGCCCCAG 124
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Indels
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Best Local Similarity 83.6%; Pred. No. 2.4e-17;
Matches 127; Conservative 0; Mismatches 24
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Location/Qualifiers
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/db_xref="taxon:10090"
/clone="IMAGE:332741"
/db_xref="taxon:10090"
/clone="IMAGE:697936"
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                                                                 /sex="mixed"
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KEYWORDS
SOURCE
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AA756051 1188 bp mRNA linear EST 21-JAN-1998 vul1610.rl Barstead mouse myotubes MPLRB5 Mus musculus cDNA clone IMAGE:1180362 5', mRNA sequence.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Contact: Marra M/Mouse EST Project
Washh-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Par: 314 286 1810
                                                                                                                                                                                                                                                                                                                  Length 246;
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                                                                                                                                                                                                                                                                                                                  tch 35.8%; Score 97.6; DB 7; al Similarity 83.1%; Pred. No. 3.1e-16; 123; Conservative 0; Mismatches 24;
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Location/Qualifiers
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/clone="IMAGE:1180362"
/cell_line="C2C12"
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Mus musculus
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/strain="C3H"
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AW326399
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PUBMED
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mb49d03.yl Soares mouse p3NMF19.5 Mus musculus cDNA clone
IMA6E:32741 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (Info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 120)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Waterston,R., Mill,T., Jackson,Y., Cardenas,M., McCann,R., The WashU-NCT Mouse EST Project 1999
                                                                                                                                                                                                                                                                             1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG
                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                       Length 188;
                                                                                                                                                                                                                                                   21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                    35.3%; Score 96.4; DB 1;
84.5%; Pred. No. 6.3e-16;
ive 0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seg primer: -40RP from Gibco
High quality sequence stop: 119
POLYA=No.
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Matches 120;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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/organism="Mus musculus" /mol_type="mRNA"

source

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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.380904.e. Vector identified by cross_match with the -minscore 20
PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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Fahrenkrug, S.C., Smith, T.P.L., Freking, B.A., Cho, J., White, J., Vallet, J., Wise, T., Rohrer, G.A., Pertea, G., Sultana, R., Porcine gene discovery by normalized cDNA-library sequencing and EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18; Indels
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PO Box 166, Clay Center, NE 68933-0166, USA
TED: 402 762 4369
Fax: 402 762 4390
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larity 83.2%; Pred. No. 6.4e-11;
Conservative 0; Mismatches 18;
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/lab_host="DH10B"
/clone_lib="MARC_2PIG"
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
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Plate: 10 row: J column: 20
Seg primer: ATTTAGGTGACACTATAG.
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AV435580 23.0 bp mRNA linear EST 23-AUG-2000 AV435580 Porphyra yezoensis TU-1 Porphyra yezoensis cDNA clone PMC9502_r 5', mRNA sequence.
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 ATGGCAGCAAAATTCGCAACCTGCTGGGTTGGCTCTGGGTCGGTTGGAGGGCGCCAGTG 154
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                                                                                                                                                                                                                                                                                                                                                                 36 CCCAGCGCCTTCCCCAATGCCCCAGCTACCTCTGATACCCTTGAGATGCGGGTCCGAGA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:2788"
/clone="PW059e02 r"
/clone_lib="Porphyra yezoensis TU-1"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
                  thie
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Eukaryota; Rhodophyta; Bangiophyceae; Bangiales, Bangiaceae;
             by hydroxyapatite chromatography and used to make
library."
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                                                                                                                                                                                         Length 247;
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                                                                                                                                                                                                                                                                      37; Indels
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                     Query Match 12.4%; Score 33.8; DB 4; Best Local Similarity 60.2%; Pred. No. 1.3e+02; Matches 56; Conservative 0; Mismatches 37;
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/mol_type="mRNA"
/strain="TU-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGCAGCAAATTCGCAACCTGCTGGGGTTGGC 128
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Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
High quality sequence stop: 221.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillar, L., Marra, M., Pape, D., Wylle, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Glabone, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                 1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAAT
                                                                                                                                                                                                                         Score 46.6; DB 2; Length 263;
Pred. No. 0.038;
0; Mismatches 4; Indels (
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/dev_stage="Adult"
/lab_host="DH10B"
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/clone="IMAGE:5673520"
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Other_ESTs: ie85a09.x1
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ilarity 92.5%;
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Tel: 617-495-1812
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completed: January 31, 2005, 20:17:10
                Porphyra yezoensis
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Matches 64; Conserv
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                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
1 (bases 1 to 220)
1 bases 1 to 220)
1 bases 1. Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
Simpson, A.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
AW818811 220 bp mRNA linear EST 17-MAY-2000 RC4-ST0279-010400-019-904 ST0279 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC4-ST0279-010
Seq primer: puc 18 forward
High quality sequence start: 36
High quality sequence store: 114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: stemach; Vector: puc18; Site 1: Smal; Site 2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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AV430042 AV430042 I GI:8585267
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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60.0%; Pred. No. 3.1e+02;
iive 0; Mismatches 36;
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/dev_stage="Adult"
/clone_lib="ST0279"
                                                                      AW818811.1 GI:7911909
                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: +55-11-2704922
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Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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/mol_type=manA"
/strain="TU-1"
/db_tref="taxon:2788"
/clone="Piol2603 r"
/clone="piol2603 r"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
Xhol:
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                                                                                                                                                                                          1 (bases 1 to 133)
Nitraido,I., Asamizu,E., Nakajima,M., Nakamura,Y., Saga,N. and
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                                                    Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae;
                                                                                                                                                                                                                                                                                                                                                                                     Generation of 10,154 expressed sequence tags from a leafy gametophyte of a marine red alga, Porphyra yezoensis DNA Res. 7, 223-227 (2000)
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Pred. No. 3.3e+02;
0; Mismatches 53; Indels
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Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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Porphyra yezoensis
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Probe Human

Aak23818 Human bra
Abs4546 Human liv
Abs23400 Human liv
Abs41025 Fusarium
Abs41025 Probe #19
Abc14594 Pseudomon
Aax51903 Human ova
Ac694768 Human col
Abr80318 Corn earAch86002 Human gen
Ach86002 Human sig

ABT14594 AAX51903 ABL80211 ACD94768 ADH31736

ABS23400 AAF10329 ABA41025

AAK23818 ABS49548

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		·	77	4.07
	GenCore version 5.1.6	U	23	26.4
	Copyright (c) 1993 - 2005 Compugen Ltd.	υ	24	26.4
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		υ	56	26.4
OM nucleic - nu	OM nucleic - nucleic search, using sw model	O	27	26.2
		U	28	56
Run on:	January 31, 2005, 18:07:55 ; Search time 317 Seconds	O	29	26
	(without alignments)	O	30	25.8
	4520.795 Million cell updates/sec		31	25.8
		U	32	25.8
Title:	US-10-057-813-13_COPY_1_273		33	25.6
Perfect score:	273	O	34	25.6
Sequence:	1 atggagcactaccggaaagcccaagctacgtttccttcag 273	U	35	25.6
		U	36	25.6
Scoring table:			37	25.4
	Gapop 10.0 , Gapext 1.0		38	25.4
			39	25.4
Searched:	4134886 segs, 2624710521 residues	O	40	25.4
			41	25.4
Total number of	Total number of hits satisfying chosen parameters: 4923180	υ	42	25.2
		O	43	25.2
Minimum DB seq length: 0	length: 0	O	44	25.2
Maximum DB seq	length: 273	U	45	25.2
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SITERBOOTE PROJECT	FOBL_PLOCEBBING: MILLIMUM MACCH 100*			
	Listing first 45 summaries			
Database :	N_Geneseq_23Sep04:*	RES	RESULT 1	

ALIGNMENTS

ABQ55864 standard; cDNA; 192 BP.

ABQ55864/ RESULT 1

ABQ55864;

Ach86303 Human gen Aax11982 Human bia Abx76158 Lung canc

AAC18105 ACA56063 ADI55859 ACH44670 AAZ07150

979

ACH86303

AAX11982

ADP64955

ACH95344

ACH86002

311

111988 111988 111988 111988 11198 11198 11198 11198 11198 11198

Adp64955 Human sma

Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian cancer), immune disorders, cardiovascular disorders and neurological Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndrome; PCOS; ovarian cyst; dysmenorrhoes; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; infection; cardiovascular disorder; respiratory disorder; neurological disorder; gestrointestinal disorder; urinary system disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytosteatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive; gene; ss. Human ovarian antigen HPAMQ76 cDNA, SEQ ID NO:1744. 07-JUN-2001; 2001WO-US018569 07-JUN-2000; 2000US-0209467P 22-AUG-2002 (first entry) (HUMA-) HUMAN GENOME Birse CE, Rosen CA; WPI; 2002-147878/19. P-PSDB; ABP42787 WO200200677-A1. Homo sapiens 03-JAN-2002. diseases.

Ach85301 Human gen Adf31067 Soil meta Adf31067 Soil meta Adc79052 Human lun Add67064 Human lun Ade8756 Human lun Ade8756 Human lun Ade8756 Human lun Ada15437 Probe #16 Aba39062 Probe #13 Aba39062 Probe #17 Aak48603 Human bon

ADE87569 AAI26274 ABA73983 AAI54432

264 264 264 167 167 167 167 167

0.001 0.001 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000

ADD67064

ABA39062 AAK48603 AAK22436

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ACH85301 ADQ91957 ADF31067 AAC79052 AAD23127

29.8 228.6 27.8 27.2 27.2 27.2 27.2

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Ach82956 Human gen Abn20543 Human ORF

Abq55864 Human ova

Description

BB

Query Match Length

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2003as:* geneseqn2003bs:*

geneseqn1980s:* geneseqn1990s:* genesedn2000s:* SUMMARIES

Claim 1; SEQ ID NO 1744; 2922pp; English

Human gen Probe #16 Human foe Probe #24

ABA75273 AAI55836 AA127005 ABS48287

bra liv

Human Human

Aai26274 E
Aba73983 H
Aai54432 E
Aai54432 E
Aak48603 E
Aak28436 E
Abs48287 E
Abs22360 E
Aba72705 E
Aba752736 A

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for

Rank DR, Hanzel DK;

Penn SG,

WPI; 2004-119264/12

The invention relates to a nucleic acid probe for measuring human gene

Claim 1; SEQ ID NO 16151; 80pp; English.

surveying tissues.

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The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to CDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polymuclectides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host calls comprishing human ovarian antigen to the sequences of the invention. The invention additionally relates to recombinant vectors and host calls comprishing human ovarian antigen of ovarian antigens of ovarian antigens and polymuclectides and polypeptides in diagnossing, treating, prognosing or preventing various ovary and/or breast related disorders. Such conditions include ovarian cancer and breast cancer, and metastatic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, calsorders (e.g., infertility, disorders of pregnancy, anovulation, calsorders, infections (e.g., chlamydia, HTV, toxoplasmosis, and toxic shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus), cardiovascular disorders, cespiratory disorders (e.g., anaemia), cardiovascular disorders, cespiratory disorders, neurological disorders, gastrointestinal disorders and urinary system disorders. Ovarian antigen polypeptides and condities which modulate ovarian antigen expression or activity. The polymuclectides may also be used in screening for compounds which conditication of individuals and in forensic analysis, and the indense disgnosis, drug targeting and phenotyping. The present sequent in disease disgnosis, drug targeting and phenotyping. The present convention, Nore: The sequence of the present of the parent of the presents of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 192 BP; 41 A; 57 C; 58 G; 36 T; 0 U; 0 Other;
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63 ACCICCIGATACCCITGAGATGCGGGTCCGAGATGGCAAAATTCGCAACCTGCTGGG 122 128 ACTITCITGIAGGCITCAGACGACGACCTTGAGGGCAGCAGGAACCACCATCCGCITTT 0; Gaps 10.9%; Score 29.8; DB 6; Length 192; Query Match
10.94; cour. 10.85;
Best Local Similarity 58.44; Pred. No. 85;
Matches 52; Conservative 0; Mismatches 37; Indels 123 GTTGGCTCTGGTCGGTTGGAGGCCGGCA 151 rcrrcrccraggccccrccarca 40 68 ò a ò 셤

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Human; probe; 88; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
                                                          Human genome derived single exon probe #16151.
ACH82956/c
ID ACH82956 standard; DNA; 265 BP.
                                         29-JUL-2004 (first entry)
                                                                                                                   US2003194704-A1.
                                                                                                    Homo sapiens.
                         ACH82956;
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03-APR-2002; 2002US-00029386. 03-APR-2002; 2002US-00029386.

16-OCT-2003

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

Control of the invention relates to a nuclear acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide sequences in the specification, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acids sequences concing at least 8 amino acids of any of the 6888 amino acid sequences concing in the specification. The probe is a single exon probe that the fully defined in the stringency conditions to a nucleic acid molecule expressed in human cells or tissues. Also included are a spatially.

Comprising a plurality of single exon nucleic acid molecule gadressable set of single exon nucleic acid molecule or amplifiable from the plurality), a single conditions to measuring human gene expression, a wettor comprising the single exon nicroarray for measuring human gene expression, a vector comprising at least 8 conditionally with conservative amino acid substitutions, and contiguous amino acids of any of the above mentioned amino acid or contiguous amino acids of any of the above mentioned amino acid contiguous amino acids of any of the above mentioned amino acid contiguous amino acids of any of the above mentioned amino acid or contiguous amino acids of any of the above mentioned amino acid or acustomer desiring to measure gene expression, a method of providing that binds specifically to a peptide cited above.

Complete antibody that binds specifically to a peptide cited above.

Sequences (obtionally with conservative amino acid substitutions), and acustomer desiring to measure gene expression and accomputer-readable of acustomer desiring to measure gene expression and yeis. The probes methods and achase having a plurality of records throad any second including data on the expression of a single exon microarrays.

Complete accord including data on the expression of a single exon microarray to accord to contains and the accord includes their exon, in assessing contains in the genomic alterations in the genomic alterations, in the probes are 252 TGGAGATAGAGCTTCCACAGGGCTCTCTTCATGTCCTGGTTCCTCAGGCTGTAGATGAGC 193 192 GGATTCAGCGTGGGTATGAGGTAGAGACAGCACCAGCCAAGCGCCCTTCCAGCGGG 133 62 TACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTGG 121 61 patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/seguence.html?DocID=20030194704 2 TGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAGC ö Query Match 10.5%; Score 28.6; DB 12; Length 265; Best Local Similarity 49.0%; Pred. No. 2.1e+02; Matches 76; Conservative 0; Mismatches 79; Indels 0; Sequence 265 BP; 51 A; 97 C; 60 G; 57 T; 0 U; 0 Other; 156 132 dagradcegerédredicerdrenderedadir 98 122 GGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCT ABN20543 standard; cDNA; 194 BP. 24-JUN-2002 (first entry) ABN20543; RESULT 3 ABN20543 à g 8 g ò 유

Human ORFX polynucleotide sequence SEQ ID NO:9563. 06-DEC-2001

cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; open reading frame; ORFX; gene therapy; cancer; cirrhosis; 29-MAY-2001; 2001WO-US010836 30-MAY-2000; 2000US-0206132P. 29-AUG-2000; 2000US-0228716P. myasthenia gravis; gene; ss. Shimkets RA, Leach MD; (CURA-) CURAGEN CORP. WPI; 2002-106308/14. P-PSDB; ABP04791 WO200192523-A2. Homo sapiens.

Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.

Disclosure; SEQ ID NO 9563; 1037pp; English.

The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1) in the specification). ABM15762 to ABM27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polymucleotide sequences can be used in gene therapy. ORFX sequences can be used in gene therapy. ORFX sequences can be used in the tendence of a medicament of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benigh tumours, keloid, degenerative disorders related to organ transplantation, cardiovascular diseases, disorders related to organ transplantation, cardiovascular diseases, diabetes mellitus, systemic storage disease, various immune deficiencies and disorders, infectious disease, autoimmune disorders such as multiple sclerosis, rheumatoid arthritis, autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut to protection or treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form and the printed specification, but was obtained in electronic form part of the printed specification, but was obtained in electronic. cormat directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 194 BP; 41 A; 48 C; 74 G; 30 T; 0 U; 1 Other;

Query Match

ö CTCAGGTTCTGGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCG 230 Gaps ö Score 27.8; DB 6; Length 194; 32; Indels Pred. No. 3.3e+02 0; Mismatches 3 Query Match
Best Local Similarity 59.5%;
Matches 47; Conservative 171

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CTCAGGGTCGGGGGTGGAGTAAGCAGGCAGATGAGCTGCCCTGAGATTGCTGGGAGGAG

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231 GGTCCCAGGCCTGCACCAG 249

71 GGAAGGCGGCAGACCCAG 89

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RESULT 4 ACH85301

BP. ACH85301 standard; DNA; 122 ACH85301;

(first entry) 29-JUL-2004

Human genome derived single exon probe #18496.

Human; probe; 88; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.

Homo sapiens.

US2003194704-A1.

16-OCT-2003.

03-APR-2002; 2002US-00029386.

03-APR-2002; 2002US-00029386.

(PENN/) PENN S G. (RANK/) RANK D R. (HANZ/) HANZEL D K.

Penn SG, Rank DR, Hanzel DK;

WPI; 2004-119264/12.

New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for surveying tissues.

Claim 1; SEQ ID NO 18496; 80pp; English.

The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide expression, comprising any of the 27,400 fully defined nucleotide expression, or their complements or fragments, and encoding at least 8 amino acids of any of the 6888 amino acid sequences fully defined in the specification. The probe is a single exon probe that hybridises under high stringency conditions to a nucleic acid molecule expression (comprising a plurality of single exon nucleic acid molecule or addressable set of single exon nucleic acid probes for measuring human cells or amplifiable from the plurality), a single comparately and addressably isolatable or amplifiable from the plurality), a single exon microarray for measuring human gene expression, a wetto comprising the single exon probe cited above, an ORF-encoded peptide comprising at least 8 contiguous amino acids of any of the above- mentioned amino acid of supervalve amino acid and/or licensing single exon probes or microarrays to measure gene expression, a method of solated antibody that binds specifically to a peptide cited above, manno gene expression, a method of such a customer desling and/or licensing single exon probes or microarrays to the corage medium which contains a database having a plurality of records cach record including data on the expression of a single exon probe cited above. The probe, methods and apparatus are useful in gene expression analysis. The probes methods and apparatus are useful in gene expression analysis. The probes methods and apparatus are useful in dene expression analysis. The probes methods and apparatus are useful in dene expression analysis. specific exon, or in constructing genome-derived single exon microarrays. In addition, the probes are used in identifying and characterising alternative splicing events, in detecting and characterising gross alterations in the genomic locus that includes their exon, in assessing smaller genomic alterations, in priming the synthesis of nucleic acids, or in expressing the ORF-encoded peptide. The present sequence is a human single exon probe of the invention. Note: The sequence data for this

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                                                                                                                           CTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTTGTAGTTCTCAGGTTCTGGCAGGG 187
                                                                                                                                                                                                                                                                                                                                                                  Dog; DRD4; intron 2; dopamine receptor D4; dog candidate; seeing-eye dog; disaster rescue dog; assisting dog; narcotics detection dog; police dog; animal herding dog; hunting dog; watchdog; housedog; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides and polypeptides, useful for screening useful dog candidates having genetic aptitudes beneficial to people, or for screening probes or identifying probes used in southern hybridization or
patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030194704
                                                                                                       Gaps
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                                                                             DB 12; Length 122;
                                                                          Score 27.6; DB 12; Length 1
Pred. No. 3.3e+02;
0; Mismatches 34; Indels
                                                 Sequence 122 BP; 17 A; 31 C; 39 G; 35 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                           Dog dopamine receptor D4, DRD4, intron 2 long form.
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                                                                                                                                                                             188 CTGCAGGAAAGGCTGTCAGCTG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                    61 Accercacececiciencies 82
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                                                                            10.1%;
58.5%;
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                                                                                     Best Local Similarity 58.5
Matches 48, Conservative
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cc sof a dog dopamine receptor D4 gene, breeding useful dog candidates that uses a dog in which the genotype of the allele in exon 1 or intron 2 of a dog dopamine receptor D4 gene is homozypetic for at least one of the parent dogs and a useful dog candidate that is selected based on the parent dogs and a useful dog candidate that is selected based on the genotype of the allele in exon 1 or intron 2 of a dog dopamine receptor 04 gene. The service dogs are seeing-eye dogs, disaster rescue dogs, assisting dogs, narcotics detection dogs, police dogs for the hearing impaired, animal herding dogs, or hunting dogs. The dogs with comparing the short form of exon 1 are watchdogs or housedogs. Dogs having the short form of intron 2 display mild-mannered behavioural traits and dogs having the long form of intron 2 display aggressive behavioural traits. The polynucleotides and polypeptides are useful for screening useful dog candidates having genetic aptitudes beneficial to companie the probes used in southern hybridisation, northern department of dopamine receptor D4, DRD4, intron 2 long form.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197 AGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTCCCAGGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 GGGCGGCCAGGCGGGCCTGGCGGGGGGGGGGGGCCGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 133 BP; 7 A; 83 C; 35 G; 8 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.4e+02;
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0; Mismatches
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ADF31067 standard; DNA; 235 BP.
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53.8%;
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Matches 56; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADF31067,
                    The invention relates to a polynucleotide derived from dog dopamine receptor D4 (DRD4) comprising the short and long forms of exon 1 (ADQ91952 and ADQ91954) or the deleted portion from the long form ADQ91950), and the short and long forms of intron 2 (ADQ91957and ADQ91958 or the deleted portion of the long form (ADQ91956). Also included are a transformant in which a polynucleotide is expressively introduced that contains a nucleotide sequence selected from ADQ91950, ADQ91952, ADQ91954, ADQ91955, ADQ91957 and ADQ91958, a polypeptide containing an amino acid sequence encoded by the above nucleic acids (ADQ91953 or ADQ91955, screening for useful dog candidates, a kit for screening for useful dog candidates comprising a pair of PCR primers that bonds to the vicinity of both terminals of an allele in exon 1 or intron
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(first entry)
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                                                                                                                                                                                                            Conservative
                                                                          especially. lung cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lodes MJ,
                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                            51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAD23127;
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                                                                                                                                                               Query Match
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together, especially for developing new enzymes; (ii) in washing and cleaning compositions for textiles or hard surfaces; (iii) for treating arm materials and intermediates in preparation of textiles, especially desizing of cotton; (iv) for starch liquefaction, especially in ethanol production; (v) for preparation of linear and/or short-chain oligosaccharides; (vi) for hydrollysis of cyclodextrins; (vii) for compounds from polysaccharide complexes or cyclodextrins; (viii) in preparation of foods and animal feeds, e.g. as antistaling additives for bread; (ix) for destroying starch-based and the same and (x) as temporary adhesives. Nucleic acid encoding the novel glycosyl hydrolases and their derivatives can be fused to other nucleic acid, especially for development of new enzymes. This sequence encodes a soil metagenome glycosyl hydrolase homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                               115 CTGCTGGGGTTGGCTCTGGGTCGGTTGGAGGCGGCAGTGCTCGGCATGTAGTGTTCTCA 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCGCTGTTCGAGCAGCTGCTGTTGGCCACCGAGCCGTCGCGAGCAGCAGCCGCTGGTA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel lung tumor polypeptides and polynucleotides, useful for detecting monitoring or treating cancer, especially lung cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is given in a specification relating to compounds for therapy and diagnosis of lung cancer. Polypeptides comprising at least an immunogenic part of a lung tumour protein are disclosed. The polypeptides are useful for inhibiting the development of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGTTCTGGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTC
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 235;
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                                                                                                                                                                                                                                                                                                                                                                                                      68; Indels
                                                                                                                                                                                                                                                                                                                Sequence 235 BP; 43 A; 88 C; 72 G; 32 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                         Score 27.2; DB 10
Pred. No. 5.1e+02;
0; Mismatches 68
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99US-00370838.
99US-00476235.
                                                                                                                                                                                                                                                                                                                                                       10.0%;
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                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 50.03
108 68; Conservative
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                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 GGTTCTGGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 especially lung cancer. Samples of T cells expressing the polypeptides may be used to inhibit the development of cancer. The polypeptides are also useful for detecting and monitoring the progression of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; lung tumour protein; immunostimulant; cytostatic; gene therapy; antisense-therapy; vaccine; immune response; lung cancer; L164Cl.cons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indirias
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SP, Algate PA, Elliot M, Mannion J,
                                                                                                                                                                                                                                                                                 9.9%; Score 27; DB 3; Length 264; 54.3%; Pred. No. 6.1e+02;
                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                       Sequence 264 BP; 52 A; 69 C; 63 G; 74 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 264 BP; 52 A; 69 C; 63 G; 74 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 ACAGGCGTGAGCCACTGCGCCCGGCCTCTTCTCC 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             235 CCAGGCCTGCACCAGCTCACCAAGCTACGTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lung tumour-specific L164C1.cons cDNA
                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAD23127 standard; cDNA; 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-00588937.
2000US-00640878.
2000US-0234517P.
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Sequence 264 BP; 52 A; 69 C; 63 G; 74 T; 0 U; 6 Other; differential display RT-PCR relating to the invention.

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The invention relates to a novel isolated polymucleotide comprising one of 32 47-6080 base pair sequences, given in the specification, or their complements or degenerate veriants, at least 20 contiguous residues of a sequence in, or having at least 75 or 90 % identity with the isolated polymucleotide, or that hybridise with the polymucleotide. The invention further comprises: an isolated polymeptide; an expression vector comprising the polymucleotide operably linked to an expression control sequence; a host cell transformed or transfected with the expression control vector; an isolated antibody or its antigen-binding fragment that specifically binds to the polymptide; a method for detecting the polymptide; an objayoutleotide that hybridises to the isolated coll population; a composition conditions; a method for stimulating and/or expanding T cells specific for a tumour protein; a stimulating of carriers and immunostimulants and a second component; a method for stimulating an immuno response in a patient; a method for retaining cancer in a patient; a method for parient: a patient of the composition of the parient of the parient of the composition of the parient of the parient of the composition of the parient of the composition of the parient of the parient of the 
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                                                                                             175 GGTTCTGGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTC 234
                                                                                                                                          12 GGATGGGGCACGGGACACATMGACTTTAACTGCCCCCACGTTNTCWAGGAAAGGATT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression control; cancer; T cell; tumour; immune; cytostatic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polynucleotide and polypeptide, useful for preparing a composition diagnosing, treating or preventing cancer.
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lung tumour-specific cDNA isolated 3' sequence, SEQ ID No 7.
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       Length 264;
                         6.1e+02;
ches 42; Indels
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                                                                                                                                                                                             235 CCAGGCCTGCACCAGCTCACCAAGCTACGTTTCC 268
                                                                                                                                                                                                                                     72 ACAGGCGTGAGCCACTGCGCCCGGCCTCTTCTCC 105
       DB 4;
  Score 27; DB 4
Pred. No. 6.1e+
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; SEQ ID NO 7; 494pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human; lung tumour-specific; ss.
                                                                                                                                                                                                                                                                                                                                                               ADD67064 standard; cDNA; 264 BP
9.9%;
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                                                  51; Conservative
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                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                               ADD67064;
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  Query Match
                      Best_Local
Matches 5
                                                                                                                                                                                                                                                                                                                    RESULT 9
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patient; a diagnostic kit comprising at least one oligonuclectide or antibody and a detection reagent comprising a reporter group; and a method for inhibiting the development of cancer in a patient. The compositions of the invention have cytostatic activity and can be used to create a vaccine. The isolated polynuclectide is useful for preparing a composition for diagnosing, treating or preventing cancer. This polynuclectide sequence represents an isolated 3' sequence used in the preparation of human lung tumour-specific cDNA sequences using

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The invention relates to polynuclectides encoding lung tumour antigens. The invention also relates to the polypeptides encoded by the polynuclectides, isolated antibodies or antigen-binding fragments that specifically bind the polypeptides and a method for detecting cancer in a patient, comprising obtaining a biological sample from the patient, contacting the sample with a binding agent that binds a polypeptide of the invention, detecting in the sample an amount of polypeptide that brinds to the binding agent, and comparing the amount of polypeptide to a predetermined cut-off value. T cells specific for a tumour protein can be stimulated and/or expanded by contacting the T cells with a polypeptide, polymucleotide or an antigen-presenting cell that expresses a
                                                            175 GGTTCTGGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTC 234
                                                                                12 GGATGGGGCCACGGAGCACAGATMGACTTTAACTGCCCCCACGTTNTCMAGGAAGGATT 71
                                                                                                                                                                                                                                                                                                                                                            luman; lung tumour antigen; gene; ss; cancer; lung cancer; CD4+; CD8+;
cell; immune response; immunostimulant; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encode lung tumor antigens and are useful to
stimulate an immune response or detect or treat a cancer in a patient,
                                Gaps
                                ö
Length 264;
                               42; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mcneill PD;
Score 27; DB 10;
Pred. No. 6.1e+02;
                                                                                                                         235 CCAGGCCTGCACCAGCTCACCAAGCTACGTTTCC 268
                                                                                                                                                     72 AcAddcardadcharaccadcarcricric 105
                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fan L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; SEQ ID NO 7; 63pp; English.
                                                                                                                                                                                                                                                                                                                             Human lung tumour antigen cDNA #7.
                                                                                                                                                                                                                                  ADE87569 standard; cDNA; 264 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-00518809.
2000US-00538037.
2000US-00588937.
2000US-00640878.
9.9%;
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2000US-00738973.
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                                                                                                                                                                                                                                                                                              29-JAN-2004 (first entry)
             Local Similarity 54.3 es 51, Conservative
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particularly lung cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                         Human; lung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-MAR-2000;
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14-DEC-2000;
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30-DEC-1999
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Query Match
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polypeptide. Cancer development can be inhibited by incubating CD4+ and/or CD8+ T cells isolated from a patient with a polypeptide, polynucleotide or an antigen-presenting cell that expresses a polypeptide, so that the T cells proliferate. The invention is used to stimulate an immune response or to detect or treat a cancer in a patient, particularly lung cancer. This sequence represents human lung tumour antigen cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                      175 GGTTCTGGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGGTC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cencer. Note: The sequence data for this patent did not form part of the printed specification, but was
                                                                                                                                                                                                                      GGATGGGGCACGGAGCACAGATMGACTTTAACTGCCCCCCACGTTNTCMAGGAAAGGATT 71
                                                                                                                                                                                                                                                                                                                                                                                                                        Probe #16207 for gene expression analysis in human cervical cell sample.
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 human; microarray; gene expression; cervical epithelial cell;
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                                                                                                                                                    Score 27; DB 10; Length 264;
Pred. No. 6.1e+02;
1; Mismatches 42; Indels
                                                                                                                              Sequence 264 BP; 52 A; 69 C; 63 G; 74 T; 0 U; 6 Other;
                                                                                                                                                                                                                                                                              72 ACAGGCGTGAGCCACTGCGCCCGGCCTCTTCTCC 105
                                                                                                                                                                                                                                                      235 CCAGGCCTGCACCAGCTCACCAAGCTACGTTTCC
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2000US-00608408.
2000US-00632366.
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2000US-0236359P.
2000GB-00024263.
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                                                                                                                                         Query Match
Best Local Similarity 54.3%
These 51; Conservative
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; foetal liver; gene expression; single exon nucleic acid probe; ss
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Pred. No. 8e+02;
0; Mismatches 21; Indels 0
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Pred. No. 8e+02;
0; Mismatches 21; Indels
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Seguence 167 BP; 19 A; 53 C; 52 G; 43 T; 0 U; 0 Other;
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2000US-0234687P.
2000US-0236359P.
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                                                                                                             9.7%;
Local Similarity 65.0%;
les 39; Conservative
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21-SEP-2000;
27-SEP-2000;
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26-MAY-2000;
30-JUN-2000;
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RESULT 13

AAI5443;

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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, seraging, monitoring and prognosing diseases of the human heart and vaccular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form at directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                      Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
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                                                                                                                                                                                                                                                                                                                 Rank
                                                                                                                                   26-MAY-2000; 2000US-0207456P.
30-UTN-2000; 2000US-0060B408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023599P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                               Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAK48603 standard; DNA; 167 BP
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
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Best Local Similarity 65.0
Matches 39; Conservative
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  WO200157274-A2
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                                      09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 CCTGCTGGGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGTGTTCTC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Probe #23118 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene expression; heart; microarray; vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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0; Mismatches 21; Indels
                                                                                                                                                                                    Probe; microarray; human; placenta; antenatal diagnosis; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 167 BP; 19 A; 53 C; 52 G; 43 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; SEQ ID NO 23118; 654pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.7%; Score 26.4;
65.0%; Pred. No. 8e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression in human placenta.
                            AAI54432 standard; DNA; 167 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
7-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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2000US-00608408
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                                                                                                         (first entry)
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les 39; Conserv
                                                                                                                                                                                                                                                                                 WO200157272-A2.
                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-2000;
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Query Match

Best Loca Matches

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173 84

Gaps

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0; Gaps

9.7%; Score 26.4; DB 4; Length 167; 65.0%; Pred. No. 8e+02; atrive 0; Mismatches 21; Indels 0

Query Match 9.7 Best Local Similarity 65.0 Matches 39; Conservative Search completed: January 31, 2005, 19:14:11 Job time : 320 secs

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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

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6: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*

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12: /cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

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18: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

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10: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

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16: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4300275 seqs, 2872944193 residues
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Maximum Match 100%
Listing first 45 summaries
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273
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 273
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		1744, AD	27866, Ā	16151, A	25556, A	5913, Ap	5913, Ap	43846, A	21806, A	24157, A	24157, A	18496, A	19299, A
	u O	e 17											e 19
	Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
		10-264-049-1744	10-719-993-27866	10-029-386-16151	10-741-601-25556	10-242-535A-5913	10-085-783A-5913	US-10-425-115-43846	10-767-701-21806	10-242-535A-24157	10-085-783A-24157	10-029-386-18496	JS-10-741-601-19299
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ф	Query Match	10.9	10.5	10.5	10.4	10.4	10.4	10.3	10.3	10.2	10.2	10.1	10.1
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Sequence 5913, Application US/10242535A;
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICAMY: Chondrodene Inc.
APPLICAMY: Chondrodene Inc.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT APPLICATION NUMBER: US 10/095,783
FRIOR APPLICATION NUMBER: US 60/305,340
FRIOR FILING DATE: 2002-02-28
FRIOR FILING DATE: 2001-07-13
FRIOR APPLICATION NUMBER: US 60/275,017
FRIOR APPLICATION NUMBER: US 60/271,955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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62 TACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAAAATTCGCAACCTGCTGG 121
                                                                                         192 GGATTCAGGGTGGGTATGAGGATGGAGTAGAGAGCAGCAGCGCCCTTCCAGCGGG 133
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US-10-741-601-25556

Sequence 25556, Application US/10741601

Sequence 25556, Application US/10741601

Sequence 25556, Application US/10741601

Sequence 25556

Sequence 25556
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Pred. No. 31;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
10.4%; Score 28.4; DE
Best Local Similarity 58.1%; Pred. No. 32;
Matches 50; Conservative 0; Mismatches
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Best Local Similarity 51.74
Matches 62; Conservative
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SOFTWARE: Patentin version (
SEQ ID NO 5913
LENGTH: 262
                                                                                                                                                                                            122 GGTTGGCTCTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
CAGANISM: Homo sapiens
US-10-741-601-25556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-242-535A-5913/c
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Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HADZEL, DAVID R.
APPLICANT: HADZEL, DAVID R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR (TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUMBER: 2001-12-20
CURRENT APPLICATION NUMBER: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine Vers. 1.1
SEQ ID NO 16151
LENGTH: 265
         Sequence 27866, Application US/10719993
Publication No. US20040265849A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FRANKE PRANKE OF WINDOWS VERSION 4.0
SEQ ID NO 27866
LENGTH: 201
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N: EXPRESSED IN FETAL LIVER, SIGNAL = 4.8

N: EXPRESSED IN HELA, SIGNAL = 2.5

N: EXPRESSED IN HEART, SIGNAL = 2.5

N: EXPRESSED IN HEART, SIGNAL = 2.5

N: EXPRESSED IN HONE MARROW, SIGNAL = 2.5

N: EXPRESSED IN HONG, SIGNAL = 2.3

N: EXPRESSED IN BARIN, SIGNAL = 5.3

N: HIT: gill276076, EVALUE 6.00e-05

N: EXT HUMAN HIT: BF062364.1, EVALUE 1.00e-03

N: SWISSPROT HIT: Q9UGF6, EVALUE 5.00e-20
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Pred. No. 28;
0; Mismatches 79;
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Pred. No. 27;
1; Mismatches
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Best Local Similarity 57.6%;
Matches 49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 49.0
Matches 76; Conservative
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US-10-719-993-27866
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APPLICANT: Kovalic, David K.
APPLICANT: Edou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwal
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT PRILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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APPLICANT: Chondrodene Inc.,
APPLICANT: Chondrodene Inc.,
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/202
CURRENT APPLICATION NUMBER: US 10/085,783
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR PILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-03-28
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                                                                             164 CAACGACGACGCCATCGCCGCTGCAGACGCGGCGGCGGCGGGGTAATCGGTCGCGCGATG 105
                                                                                                                                                                              104 ACAAACGACTACGAGGCAATCGGGTTTGGCTTTGGGTCGGATCGGTCTTAAGAGTACTC 45
                                CAGCGCCTTCCCCAATGCCCCAGCTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATG 97
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OTHER INFORMATION: unsure at all n locations
FEATURE:
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Pred. No. 43;
0; Mismatches
                                                                                                                                98 GCAGCAAATTCGCAACCTGCTGGGGTTGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 24157, Application US/10242535A; Publication No. US20040013663A1; GENERAL INFORMATION:
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... Sequence 21806, Application US/10767701
... Publication No. US20040172684A1
... GENERAL INFORMATION:
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US-10-767-701-21806
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Best Local Similarity 53.2%;
Matches 58; Conservative
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                                                                                                                                                                                                                                    158 GGCA 161
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LOCATION: (1)..(
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LENGTH: 227
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APPLICANT: La ROSa, Thomas J.
APPLICANT: Shou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Jan, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 43846
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Chondrodene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2001-02-28
FRIOR APPLICATION NUMBER: US 60/305,340
FRIOR FILING DATE: 2001-07-13
FRIOR FILING DATE: 2001-07-13
FRIOR FILING DATE: 2001-02-28
FRIOR APPLICATION NUMBER: US 60/271,955
FRIOR APPLICATION NUMBER: US 60/271,955
FRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SSEQ ID NOS: 58994
SSEQ ID NOS: 58994
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ACCTCCTGATACCCTTGAGATGCGGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTGGG 122
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                                                86 ACTITICITICATAGGCITICAGACGACCITICAGGGCAGCAGGAACCACCATCGGCITITI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 16;
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US-10-425-115-43846
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Pred. No. 32;
0; Mismatches
                                                                                                     123 GTTGGCTCTGGGTCGGTTGGAGGGCG 148
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Sequence 5913, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
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Publication No. US20040214272A1
GENERAL INFORMATION:
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Best Local Similarity
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Best Local Similarity
Matches 64; Conserv
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ORGANISM: Zea mays
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US-10-085-783A-5913
63
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Sequence 24157, Application US/10085783A

Publication No. US20040037841A1

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis
FILE REPERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085,783A

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-03-12

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOUTHWARE: PatentIn version 3.2

LENGTH: 154

LENGTH: 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 ACTITCITGIAGGCITCANACGCCCGACCTINAGGCAGCAGCAGCACCATCATCGCTTT 94
                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                               Length 154;
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10.2%; Score 27.8; DB 16;
Best Local Similarity 56.2%; Pred. No. 48;
Matches 50; Conservative 0; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                             DB 16;
                                                                                                                                                                                                                                                                                                                                                                         Query Match
10.2%; Score 27.8; DE
Best Local Similarity 56.2%; Pred. No. 48;
Matches 50; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 GTTGGCTCTGGGTCGGTTGGAGGCCGGCA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 TCTTGTCGTAGGCGCGGGGATGCCGTCA 65
                                                                                                                                                                                                                                                   FEATURE:

NAME/KEY: misc feature
LOCATION: (135)...(135)

OTHER INFORMATION: n is a, c, g, or US-10-242-535A-24157
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LOCATION: (1357..(135)
OTHER INFORMATION: n is a, c, g,
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 24157
LENGTH: 154
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                                                                                         FEATURE:
NAME/KEY: misc feature
LOCATION: (2)...(3)
OTHER INFORMATION: n is a, c.
FEATURE:
NAME/KEY: misc feature
LOCATION: (122)...(122)
OTHER INFORMATION: n is a, c.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (122)..(122)
OTHER INFORMATION: n is
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                                                          TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-085-783A-24157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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Sequence 18496, Application US/10029386
| Publication No. US20030194704A1
| GENERAL INFORMATION:
| APPLICANT: Renn, Sharron G. |
| APPLICANT: Renn, Sharron G. |
| APPLICANT: Rank, David R. |
| TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR OF TITLE OF INVENTION: EXPRESSION ANALYSIS TWO |
| TITLE OF INVENTION: EXPRESSION ANALYSIS TWO |
| TITLE OF INVENTION: EXPRESSION ANALYSIS TWO |
| TITLE OF INVENTION: BAPPLICATION NUMBER: US/10/029,386 |
| CURRENT FILING DATE: 2001-12-20 |
| NUMBER OF SEQ ID NOS: 34288 |
| SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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63 ACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTGGG 122
                                            153 ACTITCITGIAGGCITCANACGCCCGACCTINAGGGCAGCAGGACCCACCATCGCTITT 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTAGGATTCAGGTCGAATTCCGCGATGATCGCCTGCTGCAAGCCCAGGTTCTTACAGGA 60
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Publication No. US20040166519A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REPRENCE: CL001500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT PILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FRAESEQ for Windows Version 4.0
IEBNGTH: 201
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.8

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.5

OTHER INFORMATION: SWISSENCY HIT: P46729, EVALUE 7.90e+00

OTHER INFORMATION: EST HUMAN HIT: BE615665.1, EVALUE 1.50e-01

OTHER INFORMATION: NT HIT: AF144523.1, EVALUE 1.00e-01
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0; Mismatches
                                                                                                                     123 GTTGGCTCTGGGTCGGTTGGAGGGCGGCA 151
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10.1%; Score 27.6;
Best Local Similarity 60.8%; Pred. No. 57
Matches 45; Conservative 0; Mismatche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 ACGCTGACCGGGCTGTCTGCTG 82
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ORGANISM: Homo sapiens
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CORGANISM: Homo sapiens
US-10-741-601-19299
                                                                                                                                                                                                                                                                                                         US-10-029-386-18496
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completed: January 31, 2005, 21:07:51
he : 339 secs
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ORGANISM: Synechocystis sp
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Matches 68; Conservative
                                                                                                                                                                                                                                                                            US-10-872-874-287/c
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    GGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGTCCCAGGCCTGCACCAGCTCACCAA 257
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Sequence 23785, Application US/10741601
Fublication No. US20040166519A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENERIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
TITLE REPRENCE: CLOO1500
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SEQ ID NO 23785
LENGTH: 201
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Publication No. US20040121368A1
GENERAL INFORMATION:
TITLE OF INVENTION: Polynuclectides, polypeptides and method for TITLE OF INVENTION: Screening for useful dog candidates.
TITLE OF INVENTION: Screening for useful dog candidates.
TITLE OF INVENTION: BOLYDUCATION NUMBER: US/10/641,428
CURRENT APPLICATION NUMBER: US/10/641,428
PRIOR APPLICATION NUMBER: US/10/641,428
PRIOR FILING DATE: 2003-08-15
PRIOR FILING DATE: 2002-12-24
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
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10.1%; Score 27.6; DB 17; Length 201;
Best Local Similarity 60.8%; Pred. No. 57;
Matches 45; Conservative 0; Mismatches 29; Indels 0
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LOCATION: (1)..(133)
OTHER INFORMATION: Dopamine Receptor D4 Intron 2 (Long form)
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Pred. No. 74;
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53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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US-10-741-601-23785
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Best Local Similarity
Matches 56; Conserval
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198
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115 CTGCTGGGGTTGGCTTGGAGGGGGGGCAGTGCTCGGCATGTAGTGTTCTCA 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145 GGGGTGTTCGAGCAGCAGGTGCTGTTGGCCACCGAGCCGTCGCGAGCAGCAGCCGCTGGTA 86
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197 AGGCTGTCACCTGCCTGAGATTGTCAAGCGCCGGGTCCCAGGC 240
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                                              Score 27.2; DB 18;
Pred. No. 79;
0; Mismatches 68;
                                                                                                                                                                                                                                                     APPLICANT: Breves, Roland
APPLICANT: Breves, Roland
APPLICANT: Breves, Rall-Heinz
APPLICANT: Care, Jurgen
APPLICANT: Lorenz, Patrick
APPLICANT: Lorenz, Patrick
APPLICANT: Zinke, Holger
TILE OF INVENTION: GLYCCSYL HYDROLASES
FILE REPERENCE: HENK-0088 / H 5206
CURRENT APPLICATION NUMBER: US/10/872,874
CURRENT FILING DATE: 2004-06-21
PRIOR PILING DATE: 2002-12-13
PRIOR PILING DATE: 2001-12-11
NUMBER OF SEQ ID NOS: 320
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEG ID NO 287
                                                                                                                                                                             ; Sequence 287, Application US/10872874; Publication No. US20050003419A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.0%;
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1001:
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                            January 31, 2005, 19:01:47 ; Search time 2458 Seconds (without alignments) 4503.816 Million cell updates/sec
                                               US-10-057-813-13_COPY_1_273
273
1 atggagcactaccggaaagc......ccaagctacgttccttcag 273
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Compugen Ltd.
                                                                                  44308572 seqs, 20275418765 residues
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Copyright (c) 1993 - 2005
                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                   - nucleic search, using sw model
                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                     seq length: 0
seq length: 273
                                                      Perfect score:
                                                                    Scoring table:
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Maximum DB s
                   OM nucleic
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                                                          Sequence:
                                                                                  Searched:
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/cgn2_6/ptodata/1/pna/US6057_COMB.seq:*
/cgn2_6/ptodata/1/pna/US6058_COMB.seq:*
```

APPLICANT: Stuve, Laura L.

APPLICANT: Stuart, Susan G.

APPLICANT: Ito, Laura V.

APPLICANT: Akerblom, Ingrid B.

APPLICANT: Delegeanc, Angelo M.

APPLICANT: Nedegeanc, Angelo M.

APPLICANT: Naughton, Rebeca E.

APPLICANT: Kingler, Tod M.

APPLICANT: Kingler, Tod M.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: SIGNOID ADENOCARCINOMA

Gooding, Douglas H.

SSEE: INCYTE PHARMACEUTICALS, INC.
7: 3174 PORTER DRIVE
PALO ALTO
CALIFORNIA

STATE: CA STREET:

CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PH

COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERCEC 6.1 for Windows/MS-DOS 6.2
SOFTWARE: WORD PERCEC 6.1 for Windows/MS-DOS 6.2
SOFTWARE: WORD PERCEC 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/856,624
FILING DATE: MAY 13, 1996
FILING DATE: MAY 13, 1996
FILING DATE: MAY 13, 1996
ATTORNEY/AGENT INFORMATION:
MANNEY/AGENT INFORMATION:
MANNEY/AGENT INFORMATION:
MANNEY/AGENT INFORMATION:
MANNEY/AGENT INFORMATION:
MANNEY/AGENT INFORMATION:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Ap	Ap.	AD.	۰4	βp	٠,	App	A	A	A	44	Ap	Ap	Α.	A	Ap	, Æ	Ø	4	Ap	Α,	Ap	4	lac	A	4	Tac	Ap	Ap	. 6 . 6	Ap	4	Ap	A	Š	ď	A	Ø	Ø	4	4	Ap	Αp	Ap	×
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	Length	264	9	7	7	4	4	9	9	9	9	262	9	S	S	ß	ß	S	LO.	'n	4	℧	4	o	m	3	3	m	m	m	233	10	10		~	~	\sim	\sim	\sim	\sim	$^{\circ}$	\sim	~	~	210	_
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NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 9,132
TELECOMUNICATION INFORMATION:
TELEPACH (415) 845-4166
INFORMATION FOR SEQ ID NO: 2456:
SEQUENCE CHARACTERISTICS:
LENGTH: 264 Dase pairs

ALIGNMENTS

ö 107 120 108 TCGCAACTGCTGGGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGT 167 121 GTTCTCAGGTTCTGGCAGGGCTGCAGAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCG 180 GITCTCAGGITCTGGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCG 227 9 48 CCCAATGCCCCAGCTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAAT 1 CCCAATGCCCCAGCTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGCGCAGCAAAAT 61 TCGCAACCTGCTGGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGT Gaps ö 82.8%; Score 226; DB 13; Length 264; 100.0%; Pred. No. 6.4e-51; GCGGGTCCCAGGCCTGCACCAGCTCCAAGCTACGTTTCCTTCAG 273 GCGGGTCCCAGGCCTGCACCAGCTCACCAACGTTTCCTTCAG 226 Indels ö 100.0%; Pred. ... Query Match 82.8 Best Local Similarity 100. Matches 226; Conservative TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA IMMEDIATE SOURCE: CLONE: 1929519 US-08-856-624-2456 228 168 181 ò 셤 ò 셤 ò ద ò 셤

RESULT

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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
CLONE: 1794787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-941-869A-2841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TCGCAACCTGCTGGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GTTCTCAGGTTCTGGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGGTTGTCAAGCG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Gooding, Douglas H.

APPLICANT: Stuart, Susan G.

APPLICANT: Stuart, Susan G.

APPLICANT: Stuart, Susan G.

APPLICANT: Ito, Laura Y.

APPLICANT: Ito, Laura Y.

APPLICANT: Ito, Laura Y.

APPLICANT: Manghton, Rebecca E.

APPLICANT: Naughton, Rebecca E.

APPLICANT: Wilngler, Tod M.

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: HUMAN PROSTATE

NUMBER OF SEQUENCES: 5486

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE

CITY: PALO ALTO

STREET: GALIFORNIA

COUNTY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: TIEM PC compatible

COMPUTER: TIEM PC compatible

COMPUTER: World Perfect 6.1 for Windows/MS-DOS 6.2
                                                                APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuare J.
APPLICANT: Stuve, Laura J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mushton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF GASTROINTESTINAL SYSTEM TISSUE FILE REFERENCE: PD-1024 CID.
CURRENT FILING DATE: 2000-03-30
CURRENT FILING DATE: 2000-03-30
RRIOR APPLICATION NUMBER: US/09/540,766
CURRENT FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 77960
SOSTWARE: FERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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82.8%; Score 226; DB 24; Length 264;
Best Local Similarity 100.0%; Pred. No. 6.4e-51;
Matches 226; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 GCGGGTCCCAGGCTGCACCAGCTCAGCTACGTTTCCTTCAG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu00958497
US-09-540-766-8863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2841, Application US/08941869A GENERAL INFORMATION:
                     Sequence 8863, Application US/09540766
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-941-869A-2841
                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 8863
LENGTH: 264
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54 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 180
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APPLICANT: Seilhamer, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCEPOTIDES OF MALE REPRODUCTIVE TISSUE FILE REFERENCE: PD-102 YNUMBER: US/09/540,208
CURRENT APPLICATION UMBER: US/09/540,208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 70811 SOFTWARE: PERL Program SEQ ID NO 35269 LENGTH: 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGAT 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79.9%; Score 218; DB 14;
100.0%; Pred. No. 9.7e-49;
iive 0; Mismatches 0;
                                                                         CLASSIFICATION 1435
PURIOR PAPLICATION DATA:
APPLICATION NUMBER: 60/027,839
FILING DATE: SEPTEMBER 30, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/012,689
FILING DATE: FEBRUARY 27, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0119-1 US
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 2841:
SEQUENCE CHARACTERISTICS:
LEMETH: 271 base pairs
TYPE: NUCleic acid
TYPE: NUCleic acid
TYPE: NUCleic acid
APPLICATION NUMBER: US/08/941,869A
FILING DATE: HEREWITH
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 4
10.09-540-208-35269
1 Sequence 35269, Application US/09540208
1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 218; Conservative
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us-10-057-813-13_copy_1_273.closed.rnpm

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61 CTACCICCIGATACCCTIGAGAIGCGGGTCCGAGAIGGCAGAAATICGCAACCIGCTG 120
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CURRENT APPLICATION NUMBER: 09/008,119
FRIOR PAPLICATION NUMBER: 09/008,119
FRIOR PAPLICATION NUMBER: 09/008,119
FRIOR PAPLICATION NUMBER: 09/008,119
FRIOR PAPLICATION NUMBER: 09/008,119
FRIOR APPLICATION NUMBER: 07/977,780
FRIOR APPLICATION NUMBER: 07/916,491
FRIOR APPLICATION NUMBER: 07/916,491
FRIOR APPLICATION NUMBER: 07/916,491
FRIOR PILING DATE: 1992-07-17
FRIOR APPLICATION NUMBER: 08/138,571
FRIOR PILING DATE: 1995-05-10
FRIOR FILING DATE: 1994-07-26
FRIOR APPLICATION NUMBER: 08/196,364
FRIOR PILING DATE: 1994-02-14
FRIOR APPLICATION NUMBER: 08/196,364
FRIOR APPLICATION NUMBER: 08/196,364
FRIOR PILING DATE: 1994-02-14
FRIOR PILING DATE: 1994-02-14
FRIOR PILING DATE: 1994-02-14
FRIOR PILING DATE: 1994-02-14
FRIOR FILING DATE: 1994-02-14
FRIOR FILING DATE: 1994-03-14
FRIOR FILING DATE: 1995-05-05
FRIOR 
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Sequence 126181, Application US/09540233D

GENERAL INFORMATION:
APPLICANT: Scilhamer, Jeffrey J.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Rebecca B.
TITLE OF INVENTION: POLYNUCLEOTIDES OF HEMIC AND IMMUNE SYSTEM TISSUE
FILE REPERENCE: PD-1030 CIP
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                                                                                                                                                                                                                                                    Score 212; DB 9; Length 245;
Pred. No. 4.1e-47;
0; Mismatches 4; Indels
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OTHER INFORMATION: Incyte ID No: hu00448643
                                                                                                                                                                                                                                               77.78;
98.18;
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LOCATION: 103, 105, 178, 231
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 98.17
Matches 212; Conservative
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ORGANISM: Homo sapiens
                       CDNA
                   ; MOLECULE TYPE: cDN;
; IMMEDIATE SOURCE:
; CLONE: P-033488
US-08-438-571A-2389
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LENGTH: 245
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NT: Seilhamer, Jeffrey J.
NT: Seilhamer, Jeffrey J.
NT: Levine, Wendy B.
NT: Levine, Nicole
NT: Stuark, Susan G.
NT: Stuark, Susan G.
NT: Stuark, Susan G.
NT: Stuark, Pamel W.
NT: Bills, Pamela Kay
NT: Altus, Christina M.
NT: Altus, Christina M.
NT: Akerblow, Ingrid Brika
NT: Akerblow, Ingrid Brika
NT: Akerblow, Ingrid Brika
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0
                                                                                                                                                                                                    Length 271;
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MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURENT APPLICATION NUMBER: US/08/438,571A
PFILING DATE:
CLASSIFICATION NUMBER: US/08/438,571A
TALERENORE, MICHAEL C, Ph.D.
REGISTRATION NUMBER: PD-01-5 US
TELECOMMUNICATION INFORMATION:
TELEBRONE: (415) 845-4166
INFORMATION FOR SEQ ID NO: 2389:
SEQUENCE CHARACTERISTICS:
LENGTH: 245 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGAT 218
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                                                                                                                                                                            Query Match
79.9%; Score 218; DB 24;
Best Local Similarity 100.0%; Pred. No. 9.7e-49;
Matches 218; Conservative 0; Mismatches 0;
                                           ; OTHER INFORMATION: Incyte ID No: hu00317250
US-09-540-208-35269
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NUMBER OF SEQUENCES: 5094
CORRESPONDENCE ADDRESS: ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2389, Application US/08438571A GENERAL INFORMATION:
NAME/KEY: misc_feature
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STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-08-438-571A-2389
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APPLICANT:
APPLICANT:
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49 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCCAGCGCCTTCCCCAATGCCCCAG 108
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                                                                                                                                                                                                                                                                                                                                                                   61 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG 120
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                                                                                                                                                                                                                                                             1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGGGGCCTTCCCCAATGCCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                   109 CTACCTCCTGATACCCTTGAGATGCGGCTCCGAGATGGCCAGCAAATTCGCAACCTGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6888, Application US/09539334
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Stuart, Suara J.
APPLICANT: Stuart, Suara J.
APPLICANT: Stuart, Sara J.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF ENDOCRINE SYSTEM TISSUE FILE REFERENCE: PD-1026 CIP
CURRENT APPLICATION NUMBER: US/09/539,334
CURRENT APPLICATION DATE: 2000-03-30
"Prior application data removed - refer to PALM or file wrapper"
NUMBER OF SEQ ID NOS: 38381
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                                                                                                                                                        Length 260;
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Best Local Similarity 100.0%; Pred. No. 1.8e-45;
Matches 206; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                             0; Indels
                                                                                                                                                     Query Match 75.5%; Score 206; DB 14; Best Local Similarity 100.0%; Pred. No. 1.8e-45; Matches 206; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu00887627
US-09-539-334-6888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GGCAGGCTGCAGGAAAGGCTGTCAG 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        229 GGCAGGCTGCAGGAAAGGCTGTCAG 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                             ) MOLECULE TYPE: CDN1
; IMMEDIATE SOURCE:
; CLONE: 2071192H2
US-08-959-395-768
        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 8
US-09-539-334-6888
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SEQ ID NO 6888
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                                                                                                                                                                                                                                                                                                                                                                                   121 GGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGGCTCTGGCCATGTAGTGTTCTCAGGTTCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                           145 GGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTNCTCGGCATGTAGTGTTCTCAGGTTCT 204
                                                                                                                                                                                1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGGGGCCTTCCCCAATGCCCCAG 60
                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Gooding, Douglas H.
APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura Y.
APPLICANT: Inc, Laura Y.
APPLICANT: Delegene, Angelo M.
APPLICANT: Naviphton, Rebecca E.
APPLICANT: Ningler, Tod M.
TITLE OF INVENTION: HUMAN PANCREATIC ISLET CELLS
NUMBER OF SEQUENCES: 5789
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 9430.
                                                                                                                                                                                                                                25 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG
                                                                                                                                  Gaps
                                                                                                                                  .
0
                                                                        Query Match 77.7%; Score 212; DB 24; Length 245; Best Local Similarity 98.1%; Pred. No. 4.1e-47; Matches 212; Conservative 0; Mismatches 4; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDIE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATE: HEREWITH
CLASSIPICATION NUMBER: US/08/959,395
FILING DATE: HEREWITH
CLASSIPICATION NATA:
APPLICATION NUMBER: 60/030,755
FILING DATE: OCTOBER 28, 1996
FRIOR APPLICATION NUMBER: 60/033,551
FILING DATE: DECEMBER 20, 1996
ATTORNEY/ART INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0259 US
TELECOMMUNICATION INVERS: 39,132
REFERENCE/DOCKET NUMBER: PD-0259 US
TELECOMMUNICATION INVERS: COSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCAGGCTGCAGGAAAGCTGTCAGNTGCGCTGAG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 GGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAG 216
; OTHER INFORMATION: a, t, c, g, or other US-09-540-233D-126181
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INFORMATION FOR SEQ ID NO: 766
SEQUENCE CHARACTERISTICS:
LENGTH: 260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Query Match
71.8%;
Best Local Similarity 97.5%;
Matches 196; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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TOPOLOGY: linear
MOLECULE TYPE: CDF
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-978-620-1415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGAAAATTCGCAACCTGCTG 120
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                                                                                                                               APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Aberblom, Rebecca E.
APPLICANT: Moughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF SEQUENCES: 3896
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,505
FLING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/013,529
FLING DATE:
ATTORIES
AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: INCYTE PHARMACEUTICALS, INC 3174 PORTER DRIVE
                                                                   Sequence 1415, Application US/08812505
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 GGCAGGCTGCAGGAAAGGCT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PD.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 14. SEQUENCE CHARACTERISTICS: LENGTH: 262 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 97.5'
Matches 196; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDALL STREET: 317. CITY: PALO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDN
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RESULT 9
US-08-812-505-1415
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60 ATGGAGCACTACCGGANAGCTGGCTCTNTAGAGCTCCCCAGCGCCTTCCCCAATGCCCCAG 119
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                                                                              APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Ito, Laura Y.
APPLICANT: Lobelgeane, Angelo M.
APPLICANT: Naughton, rebecome.
APPLICANT: Naughton, Rebecome.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: HUMAN BRAIN
NUMBER OF SEQUENCES: 7797
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACCUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG
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COMPUTER READABLE FORM;

ADDITON TYPE: Floppy disk
COMPUTER READABLE FORM;

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: Wind Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
COMPATER: Word Perfect 6.1 for Windows/MS-DOS
FILING DATE: HERBWITH
CLASSIFICATION NUMBER: 60/032,151
FILING DATE: DECRMER 6, 1996
CLASSIFICATION NUMBER: 60/032,151
FILING DATE: MARCH 7, 1997
CLASSIFICATION NUMBER: 08/812,505
FILING DATE: MARCH 7, 1997
CLASSIFICATION NUMBER: 33954
FRIEDRICK PROMUNICATION INFORMATION:
NUMBER: LUTHER, BARBARA U.
REFERENCE/DOCKET NUMBER: 33954
RECIENTALION NUMBER: 33954
REFERENCE/FOCKET NUMBER: 33954
REFERENCE/FOCKET NUMBER: 660) 852-0195
INFORMATION FOR SEQ ID NO: 1415:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 base pairs
TTELEPRONE: CATALET CATALET
TTELEPRONE: CATALET
TTELEP
; Sequence 1415, Application US/08978620; GENERAL INFORMATION:
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APPLICANT: Gooding, Douglas H.
APPLICANT: Stuar, Susan G.
APPLICANT: Stuar V.
APPLICANT: Stuar Y.
APPLICANT: Ito, Laura Y.
APPLICANT: Ito, Laura Y.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Naughton, Rebecca E.
APPLICANT: Ningler Tod M.
TITLE OF INVENTION: BREAST
NUMBER OF SEQUENCES: 5970
CORRESPONDENCE ADDRESSE:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
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                                                                                                                                                                                                                      COMPUTER RADBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/60/013,529
FILING DATE:
CLASSIPICATION NUMBER: US/60/013,529
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J
REGISTRATION NUMBER: PD-0126P
TELECOMMUNICATION INFORMATION:
TELEFANORE: (415) 85-0155
TELEFAN: (415) 85-0155
TELERAX: (415) 85-0155
TELERAX: GLOB NO: 1415:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 base pairs
TYPE: nucleic acid
STRANDENESS: single
TYPE: nucleic acid
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
CLONE: RASURES: CONA
TOWNED AND SURCE:
CLONE: RASURES:
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3174 PORTER DRIVE
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Best Local Similarity 97.5
Matches 196; Conservative
                                               PALO ALTO
CALIFORNIA
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                                                    CITY: PAI
STATE: COUNTRY:
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Seilhamer, Jaffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Laura L.
APPLICANT: Nullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS
FILE REFERENCE: PD-1033 CIP
CURRENT FILING DATE: 2000-03-31
CURRENT FILING DATE: 2000-03-31
RPIOR APPLICATION ADDATE: 2000-03-31
NUMBER OF SEQ ID NOS: 193582
SOFTWARE: PERL PROGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Kingler, Tod M.
TILLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF SEQUENCES: 3896
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYPTE PROCESTANT OF THE O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature

OTHER INFORMATION: Incyte ID No: hu00691274

NAME/KEY: unsure

LOCATION: 38, 76, 87, 138, 140, 168

COTHER INFORMATION: a, t, c, g, or other
US-09-540-229-45100
                                                                                                                                                                                                                                                                                                                                                                             Sequence 45100, Application US/09540229 GENERAL INFORMATION:
                                                                                                                                  240 GGCAGGCTGCAGGAAAGGCT 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           decadederrecadadadeer 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 196; Conserv
                                                                                                                                                                                                                                                                                                                                         -09-540-229-45100
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LENGTH: 262
                                         181
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FILE REFERENCE: PD-1027 CIP
CURRENT APPLICATION NUMBER: US/09/539,806
CURRENT FILING DATE: 2000-03-30
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 48372
SOFTWARE: PERL Program
SEQ ID NO 30498
LENGTH: 250
                                                                                                                                                                                                                                                                                                                                                                        Query Match 70.7%; Score 193; DB 23; Best Local Similarity 100.0%; Pred. No. 6.2e-42; Matches 193; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
COTHER INFORMATION: Incyte ID No: hu00555791
US-09-539-806-30498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 GGCAGGCTGCAG 193
                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 30498, Application US/09539806
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffray J.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahon, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF EXOCRINE GLAND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                 COMPUTER: TEXABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/951,197
FILING DATE: HEREWITH
                                                                                                                                                                                                                                              CLASSIFICATION:
PURBA SPELICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 60/027,249
FILING DATE: OCTOBER 1, 1996
CLASSIFICATION NUMBER: 08/826,438
FILING DATE: MARCH 20, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/82,285
FILING DATE: MARCH 20, 1997
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 90/82,285
FILING DATE: MARCH 20, 1997
CLASSIFICATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 90,132
REFERENCE/DOCKET NUMBER: PD-0143-1 US
TELEFONMUNICATION INPORMATION:
TELEFONMUNICATION FOR SEQ ID NO: 5067:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: mucleic acid
STRANDEDINESS: single
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Best Local Similarity 100.0
Matches 193; Conservative
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                                                                                                                                                                                                                                         CLASSIFICATION:
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CLONE: 1997229
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58 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 117
                                                                                                               178 GGGTTGGCTCTGGGTTGGAGGCGGCAGTGCTCGCCATGTAGTGTTCTCAGGTTCT 237
                                                                                                                                                                                                                                                                                                                                                                                                        61 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG
                                                                                                                                                 121 GGGTTGGCTCTGGGTTGGAGGCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT
                         Сарв
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Length 250;
                                                                                                                                                                                                                                                                                Sequence 30498, Application US/09539806B
GENERAL INFORMATION:
APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF EXOCRINE GLAND TISSUE
                        0; Indels
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0; Gaps
                                                                                                           Query Match 70.7%; Score 193; DB 23; Length 250; Best Local Similarity 100.0%; Pred. No. 6.2e-42; Matches 193; Conservative 0; Mismatches 0; Indels (
; SEQ ID NO 30498
; LENGTH: 250
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00555791
US-09-539-8068-30498
                                                                                                                                                                                                                                                                                                                                                                     Search completed: January 31, 2005, 20:58:10 Job time : 2461 secs
                                                                                                                                                                                                                                                                                                          181 GGCAGGCTGCAG 193
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NAME/KEY: misc feature
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ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 1
US-09-370-838-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-09-854-133-7
175
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0 0 0 0 0 0 0 0 0 0 0 0
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Sequence 45, Appl
Sequence 154, Appl
Sequence 154, Appl
Sequence 2448, Ap
Sequence 21139, Ap
Sequence 661, Appl
Sequence 3531, Appl
Sequence 2518, Appl
Sequence 2518, Appl
Sequence 2518, Appl
Sequence 2953, Appl
Sequence 20847, Appl
Sequence 2750, Appl
Sequence 17624, Appl
Sequence 17624, Appl
Sequence 17624, Appl
Sequence 15097, Appl
Sequence 17624, Appl
Sequence 6, Appli
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                                                                                                                                 January 31, 2005, 19:09:11; Search time 74 Seconds (without alignments) 2622.235 Million cell updates/sec
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                                                                                                                                                                                                                                                            1 atggagcactaccggaaagc.....ccaagctacgtttccttcag
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'GqDZ 6/ptodata1/ina/5A_COMB.seq:*
'GqDZ 6/ptodata1/ina/5B_COMB.seq:*
'GqDZ 6/ptodata1/ina/6A_COMB.seq:*
'GqDZ 6/ptodata1/ina/6B_COMB.seq:*
'GqDZ 6/ptodata1/ina/BECOMB.seq:*
'GqDZ 6/ptodata1/ina/PCTUS COMB.seq:*
'GqDZ 6/ptodata1/ina/backfiles1.seq:*
                 5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-370-838-7
US-09-8154-13-7
US-09-8128-45
US-09-8128-30
US-08-905-223-154
US-09-489-0394-1399
US-09-513-999C-22180
US-09-513-999C-22180
US-09-513-999C-36531
US-09-513-999C-36531
US-09-513-999C-36531
US-09-513-999C-36531
US-09-513-999C-22891
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US-09-513-999C-22891
US-09-513-999C-22891
US-09-513-999C-22891
US-09-513-999C-22891
US-09-513-999C-20847
US-09-513-999C-217841
US-09-513-999C-217624
US-09-513-999C-15131
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US-08-420-235B-6
US-08-793-624-6
                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                  824507 segs, 355394441 residues
                 GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                             - nucleic search, using sw model
                                                                                                                                                                                                                US-10-057-813-13_COPY_1_273
273
                                                                                                                                                                                                                                                                                                     IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0 seq length: 273
                                                                                                                                                                                                                    Title:
Perfect score:
                                                                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
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No.
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12 GGATGGGGCACGGAGCACAGATMGACTTTAACTGCCCCCACGTTNTCMAGGAAAGGATT 71
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Sequence
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APPLICANT: Reed, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Secriet, Heather
TITLE OF INVENTION: COMPOUNDS FOR THERAPY AND DIAGNOSIS OF
TITLE OF INVENTION: LUNG CANNER AND METHODS FOR THEIR USE
TITLE OF INVENTION: LUNG CANNER AND METHODS FOR THEIR USE
TITLE OF INVENTION NUMBER: US/09/370,838
CURRENT APPLICATION NUMBER: US/09/370,838
CURRENT FILING DATE: 1999-00-09
EARLIER PILING DATE: 1999-04-02
NUMBER OF SEQ ID NOS: 289
SOFTWARE: FASELSEQ for Windows Version 3.0
SEQ ID NO : SEQ ID NO : LENGTH: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.9%; Score 27; DB 4; Length 264;
larity 54.3%; Pred. No. 42;
Conservative 1; Mismatches 42; Indels
PCT-US95-10194-6

US-09-621-976-19219

US-09-513-999C-12509

US-08-513-999C-12509

US-08-777-19-29

US-08-777-143-29

US-08-777-143-29

US-08-777-144-29

US-08-981-8868-29

US-09-128-026-29

US-09-128-026-29

US-09-220-616-29

US-09-230-616-29

US-09-230-616-29

US-09-230-616-29

US-09-230-616-29

US-09-230-616-29

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Patent No. 6759508;
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.;
APPLICANT: Mohamath, Raodoh
APPLICANT: Henderson, Robert A.;
APPLICANT: Benson, Darin R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 7, Application US/09370838; Patent No. 6444425; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)...(264)
OTHER INFORMATION: n = A,T,C or
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STATE: California
COUNTY: USA
ZIP: 92101-3505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC COMPALISE
OPERATING SYSTEM: Win95
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LOCATION: Complement (1)..(198)
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NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,6
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Glu-Epitope Tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: 5'
NUMBER OF SEQUENCES: 5'
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    San Diego
California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
US-08-905-223-154/c
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                                                                                                    JS-09-079-812E-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-079-812E-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175 GGTTCTGGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 GGATGGGGCACGGAGGACAGATMGACTTTAACTGCCCCCACGTTNTCMAGGAAAGGATT 71
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US-09-511-625B-45/C

Sequence 45, Application US/09511625B

Sequence 45, Application US/09511625B

Sequence 45, Application US/09511625B

GENERAL INFORMATION:
APPLICANT: Date, Danarin
APPLICANT: Patel, Darrin
APPLICANT: Patel, Darrin
APPLICANT: Patel, Darrin
APPLICANT: Patel, Darrin
APPLICANT: Pierce, Jacalyn H.
TITLE OF INVENTION: ATTENDATED AND DOMINANT NEGATIVEVARIANT
TITLE OF INVENTION: ATTENDATE: 14014,0300ul
CURRENT PELING DATE: 2000-02-23
CURRENT PELING DATE: 2000-02-23
FRIOR APPLICATION NUMBER: BC1/0598/17821
FRIOR APPLICATION NUMBER: BC1/056,075
FRIOR PELING DATE: 1998-01-05
FRIOR PILING DATE: 1998-01-05
FRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 70
SEQ ID NO 45
ILENGHARE: FRAESEQ for Windows Version 4.0
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
FILE REPERBNCE: 210121.475C10
CURRENT APPLICATION NUMBER: US/09/854,133
CURRENT FILING DATE: 2001-05-11
NUMBER OF SEQ ID NOS: 735
SOFTWARE: PASISEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 9.9%; Score 27; DB 4; Length 264; Best Local Similarity 54.3%; Pred. No. 42; Matches 51; Conservative 1; Mismatches 42; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  235 CCAGGCCTGCACCAGCTCACCAAGCTACGTTTCC 268
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LOCATION: (1)...(264)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapien
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                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 7
LENGTH: 264
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18.50g-07-5 56128-10

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51; Indele
 Score 25.6; DB 4; Length 2
Pred. No. 1.1e+02;
0; Mismatches 34; Indels
 Score 25.4; DB 4;
Pred. No. 1.2e+02;
0; Mismatches 51;
 FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
SEQ ID NOS: 14342
 187 GCTGCAGGAAAGGCTGTCAG 206
 149 ścireckesekacecreece 130
 ORGANISM: Klebsiella pneumoniae
 9.3%;
 ch
1 Similarity 57.5%;
46; Conservative
 OTHER INFORMATION: r=a or g
US-09-513-999C-22180
 OTHER INFORMATION: r=a or g
 Query Match
Best Local Similarity 52.3°
Matches 56; Conservative
 NAME/KEY: misc_feature
 ORGANISM: Homo sapiens
 NAME/KEY: misc_feature
 Query Match
Best Local Similarity
 US-09-513-999C-22180
 US-09-489-039A-1139
 LOCATION: 194
 LOCATION:
 Matches
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 Sequence 2448, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Sherman, Bradley K.
TITLE OF INVERTION: POLYNUCLECTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT PILLING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL PROGram
SEQ ID NO 2448
LENGTH: 212
 173 CAGGTTCTGGCAGGCTGCAGGAAAGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGG 232
 129 TCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGTGTTTCTCAGGTTCTGGCAGGGC 188
 130 TCTGCCGAGGTGAGCGGGCACCAGGGCTGGGCATGTACAGAGGTTAGGGTTTGGCTTTGGA
 Gaps
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 Best Local Similarity 63.9%; Score 25.8; DB 3; Length 165; Matches 39; Conservative 0; Mismatrhes ?.
 9.4%; Score 25.6; DB 4; Length 212;
62.5%; Pred. No. 1.18+02;
tive 0; Mismatches 24; Indels
 NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. 6476212 700552684H1
 LOCATION: 46..153

IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: SCORE 3.8

OTHER INFORMATION: SEQ GTDSLSFLPPCFC/CP
US-08-905-223-154
 US-09-489-039A-1139/c
; Sequence 1139, Application US/09489039A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-850
TELEPAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 154:
SEQUENCE CHARACTERISTICS:
LENGTH: 165 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
TOPOLOGY: LINRAR
 MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo Sapiens
TISSUE TYPE: Brain
 Conservative
 FEATURE:
NAME/KEY: sig_peptide
 Best Local Similarity
Matches 40; Conserv
 TYPE: DNA
ORGANISM: Zea mays
 189 TGCA 192
 US-09-313-294A-2448/c
 233 T 233
 US-09-313-294A-2448
 Query Match
 FEATURE:
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GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 ô
 127 GCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCTGGCAGG 186
 Sequence 22180, Application US/09513999C
Sequence 22180, Application US/09513999C
Fatent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Dunclert, A.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT APLICATION NUMBER: US 60/122,487
FRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 22180
LENGTH: 194
 128 CTCTGGGTCGGTTGGAGGCCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCTGGCAGGG 187
 46 CACTGTTGCCCCCGGCGAGCACCAGGACTCTGCTGGTTAGGGCTGCGCGGTCAGACAGGG 105
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 188 CTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTC 234
 106 descencerestracións de contrator de cont
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NAME/KEY: misc_feature
LOCATION: 60
OTHER INFORMATION: w=a or t
FEATURE:
 LOCATION: 183 TOTHER INFORMATION: m=a or c
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 14087
LENGTH: 211
 NAME/KEY: misc_feature
LOCATION: 35
OTHER INFORMATION: y=c or
 NAME/KEY: misc_feature
LOCATION: 132
OTHER INFORMATION: y=c
 , ORGANISM: Homo sapiens
US-09-513-999C-14087
 LOCATION: 148 TOTHER INFORMATION: r=a
 NAME/KEY: misc_feature
LOCATION: 152
 TYPE: DNA
ORGANISM: Homo sapiens
 OTHER INFORMATION: h=a
 NAME/KEY: misc_feature
 OTHER INFORMATION: r=a
 NAME/KEY: misc_feature
 NAME/KEY: misc_feature
 NAME/KEY: misc_feature
LOCATION: 204
 234 CCCAG 238
 30 CCGAG 26
 TYPE: DNA
 LOCATION:
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 RESULT 10
US-09-513-999C-14087/C
i Sequence 14087, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Diolert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT PILING DATE: 2000-02-24
; CURRENT PILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-26
 Gaps
 | Sequence 661, Application US/09016434 |
| Patent No. 6500338 |
| GENERAL INFORMATION |
| APPLICANT: Janice Au-Young |
| APPLICANT: Jeffrey J. Seilhamer |
| TILLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING |
| TITLE OF INVENTION: PATHWAY GENE EXPRESSION |
| NUMBER OF SEQUENCES: 1490 |
| CORRESPONDENCE ADDRESS: ADDRESSE: INCYTE PRIVE |
| STREET: 3174 PORTER DRIVE |
| STREET: GALIFORNIA |
| STATE: CALIFORNIA |
| COUNTRY: USA
 ö
 Query Match 9.3%; Score 25.4; DB 4; Length 235; Best Local Similarity 74.4%; Pred. No. 1.3e+02; Matches 32; Conservative 0; Mismatches 11; Indels
 160 CATGTAGTGTTCTCAGGTTCTGGCAGGCTGCAGGAAAGGCTG 202
 ZIE: 94304
COMPUTER READABLE FORM:
MEDIUM TYBER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
CUSTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CUSTRANT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
 ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION UNBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0002 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 base pairs
TYPE: mucleic acid
TYPE: mucleic acid
STRANDEDNESS: single
 HEREWITH
 FILING DATE: HEREWITH CLASSIFICATION: PRIOR APPLICATION DATA: APPLICATION NUMBER:
 LIBRARY: PROSTUT12
CLONE: 2626716
 linear
 FILING DATE:
CLASSIFICATION:
 RESULT 9
US-09-016-434-661
 US-09-016-434-661
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174 AGGTTCTGGCAGGCTGCAGGAAAGGCTGTCAGCTGAGATTGTCAAGCGGCGGGT 233
 RESULT 11
US-09-513-999C-36531/C
; Sequence 36531, Application US/09513999C
; Patent No. 678361
; GENERAL INFORMATION:
; APPLICANT: Dunas Milne Edwards, J.B.
APPLICANT: Duclert, J.Y.
; APPLICANT: Duclert, J.Y.
; PATENT OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.162.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 1999-02-26
; PRIOR FILING DATE: 1999-02-26
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: PAtent.pm
; SEQ ID NO 36531
 90 AGGCCCCGGCTGGGATGCAGGGGAGGGCCCGAAGGGGGCTGAGCTCACCAGGCTGCGGCC 31
 Gaps
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 Length 211;
Query Match 9.2%; Score 25; DB 4; Length 211 Best Local Similarity 61.5%; Pred. No. 1.6e+02; Matches 40; Conservative 0; Mismatches 25; Indels
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US-09-513-999C-15097/C

i Sequence 15097, Application US/09513999C

j Sequence 15097, Application US/09513999C

j Patent No. 6783961

j GENERAL INFORMATION:

APPLICANT: Dunas Milne Edwards, J.B.

APPLICANT: Dunas Milne Edwards, J.B.

APPLICANT: Dunas Milne Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PAPLICANT: AS 383961

CURRENT PILING DATE: 2000-02-24

PRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 15097

LEWARTH: 95
 115 CTGCTGGGGTTGGCTCTGGGTTGGAGGGGGGGCAGTGCTCGGCATGTAGTGTTCTCA 174
 69 discricario con actual de la contra dela contra de la contra dela contra de la contra del la contra del la contra del la contra de la contra del la contra de la contra de la contra del la contra de la contra de la contra de la contra del la
 158 GGCATGTAGTGTTCTCAGGTTCTGGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGA 217
 175 GGTTCTGGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCGGCGGGTC 234
 9 CTGGCCTGGCTGGCCGTGGGCAGCATGTGCCTCTTCATCGCCGGCTTTGCGGTGGGCTGG 68
 88 ércairrircacrircirrirángengaanércercagrinaagécagaagegécearchée 29
 Gapa
 Gaps
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 Score 24.6; DB 4; Length 272;
Pred. No. 2.3e+02;
0; Mismatches 74; Indels
 Score 24.4; DB 4; Length 95; Pred. No. 1.9e+02;
 36; Indels
 0; Mismatches
 CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 37,071
TELECOMMUNICATION INFORMATION:
TELEFHONE: (650) 845-4166
INFORMATION FOR SEG ID NO: 855:
SEQUENCE CHARACTERISTICS:
LENGTH: 272 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
INMEDIATE SOURCE:
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TO
CURRENT APPLICATION DATA: US/09/016,434
 129 ACAGGCATCTGCGTCCTCACCAA 151
 235 CCAGGCCTGCACCAGCTCACCAA 257
 Query Match 9.0%;
Best Local Similarity 48.3%;
Matches 69; Conservative
 8.9%;
56.1%;
 Conservative
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
 TYPE: DNA
ORGANISM: Homo sapiens
US-09-513-999C-15097
 LIBRARY: PGANNOT01
CLONE: 619240
 Query Match
Best Local Similarity
 US-09-016-434-855
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 US-09-513-999C-2518/C
US-09-513-999C-2518/C

Sequence 2518, Application US/09513999C

Patent No. 6783961

APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.

APPLICANT: Glordano, J.Y.

TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PATENT FILE OF 100-073961

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm
 ö
 132 GGGTCGGTTGGAGGCCGCCAGTGCTCGGCATGTAGTGTTCTCAGGTTCTGGCAGGGCTGC 191
 229 GGTTCTGGTACCGGCAGGCAACGTGWCGCCTGGAGTTGTCACAGATKCAGGCCTGTGGGC 170
 Gaps
 0; Gaps
 Sequence 855, Application US/09016434
Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INVYTE PHARMACEUTICALS, INC.
 ö
 219 TGTCAAGCGGGGTCCCAGGCCTGCACCAGCTCACCAAGCTACGTT 265
 211 TCTCAAGCAGCTGGGACCAGGCACGCCACCACCACCAATTT 165
 9.0%; Score 24.6; DB 4; Length 215; 70.2%; Pred. No. 2.2e+02; Live 0; Mismatches 14; Indels
 Query Match 9.2%; Score 25; DB 4; Length 255; Best Local Similarity 54.1%; Pred. No. 1.7e+02; Matches 46; Conservative 2; Mismatches 37; Indels
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 6.1 for Windows/MS-DOS 6.2
 192 AGGAAAGGCTGTCAGCTGCGCTGAG 216
 169 AGCGCTGGDCGGCGCCYCGCYTAG 145
 ; OTHER INFORMATION: w=a or t
US-09-513-999C-36531
 Best Local Similarity 70.2
Matches 33; Conservative
 ORGANISM: Homo sapiens
 ; LOCATION: 31:.213
US-09-513-999C-2518
 NAME/KEY: CDS
 US-09-016-434-855
 SEQ ID NO 2518
LENGTH: 215
 TYPE: DNA
 Query Match
 FEATURE
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MESOLI 1-33

Sequence 2953, Application US/09489039A

SERENT OF TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 2709-2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT PILING DATE: 1999-01-29

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 2953

LENGTH: 261
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 84 GCGGCTCCGAGATGGCAGCAAAATTCGCAACCTGCTGGGGTTGGCTCTGGGTCGGTTGGA 143
 24 CTCTGTAGAGCTCCCAGGCGCCTTCCCCAATGCCCCAGCTACCTCCTGATACCCTTGAGAT 83
 127 ccdecrecredrodacorreacearreandeccadrococodecreceradores
 0; Gaps
 Query Match
8.9%; Score 24.4; DB 4; Length 261;
Best Local Similarity. 47.4%; Pred. No. 2.7e+02;
Matches 73; Conservative 0; Mismatches 81; Indels
 144 GGGCGGCAGTGTCGCATGTAGTGTTCTCAGGT 177
 degrecentedeacrecacedererrreagn 34
218 TIGICAAGCGGCGGGTCCCAGG 239
 28 Argigracciócadercacade 7
 ; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2953
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Search completed: January 31, 2005, 20:59:31 Job time: 75 secs

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| AF462999 Hepatitis<br>G43380 WIAF-2096-S<br>AX89351 Sequence<br>BD034884 Sequence<br>AX388104 Sequence<br>AX998870 Sequence<br>AX042427 Sequence | AX262818 Sequence<br>AX262819 Sequence<br>CQ557469 Sequence<br>AP100963 Gerilla g<br>AB076772 Home sapi                                   | A03701 Sequence 30<br>BD022722 Mirror pl<br>AB076015 TT virus<br>AX990398 Sequence<br>AY302634 Aotus tri                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | AY189210 Human ent<br>AY189213 Human ent<br>AY189214 Human ent<br>AY189216 Human ent | U71276 Human mutan<br>U71277 Human mutan<br>CQ562156 Sequence<br>CQ562325 Sequence<br>C79684 mCP V hara |   |            | linear PAT 30-JAN-2004 |                                                                            | Craniata; Vertebrata; Euteleostomi;<br>Catarrhini; Hominidae; Homo.                                              | and diagnosis of                                                                     |                                                                                                                                                                                   |                                                                                        | Length 97;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                        | receccecatorectecat 98<br>                                                               |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | linear PAT 16-JAN-2004                                                                                                                                                          |
|--------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------|---|------------|------------------------|----------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------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| 17.6 81 14<br>17.6 120 11<br>17.4 119 6<br>17.2 91 6<br>17.2 100 6<br>17.2 104 6                                                                 | 17.2 121 6<br>17.2 121 6<br>17.1 65 6<br>17.1 65 9<br>17.1 81 9                                                                           | 17.1 89 6<br>17.1 89 14<br>17.1 100 6<br>17.1 100 9                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 17.1 115 14<br>17.1 115 14<br>17.1 116 14<br>17.1 116 14                             | 17.1 120 9 1<br>17.1 120 9 1<br>16.9 60 6<br>16.9 60 6                                                  |   | ALIGNMENTS |                        | Sequence 4678 irom Patent W00192581.<br>CQ461900<br>CQ461900.1 GI:41427519 | Homo sapiens<br>Homo sapiens<br>Eukaryota, Metazoa, Chordata, Craniata, Mammalia, Eutheria, Primates, Catarrhini | Algate, P.A., Harlocker, S.L. and Jones, R. Compositions and methods for the therapy | 92581-A 4678 06-DECATION (US)                                                                                                                                                     | 13/<br>/organism="Homo sapiens"<br>/mol_type="unassigned DNA"<br>/dh vref="taxon.9666" | ָרְיָהְיִם וְיִם בְּיִרְיִם בְּיִרְיִם בְּיִרְיִם בְּיִרְיִם בְּיִרְיִם בְּיִרְיִם בְּיִרְיִם בְּיִרְיִם בְּיִר                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 200                                    | 9 CCCAGCCTCACCTGACACAGGGCTAGACCCCTCACAGTGCGCGCCATGTGCCTGCAGT                             | 9 GTGGGTGCTCAGCCGGACCCC 123                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | AX998871<br>Seguence 10334 from Patent EP1260592.<br>AX998871                                                                                                                   |
| C 22 21.6 C 23 21.4 C 24 21.2 C 2 2 21.2 C 24 21.2 C 25 21.2 C 26 21.2 C 26 21.2                                                                 | 27<br>28<br>31<br>31<br>31                                                                                                                | 1 E E E E<br>1 E E E E<br>1 E E E E<br>1 E E E<br>1 E E E<br>1 |                                                                                      |                                                                                                         | } |            |                        | Oz                                                                         | _                                                                                                                | AUTHORS A                                                                            |                                                                                                                                                                                   | D 1000                                                                                 | ORIGIN Query Match                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | Matches '                              | Qy 39<br>Db 97                                                                           | QY 99                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | RESULT 2 AX998871 LOCUS DEFINITION 8 ACCESSION                                                                                                                                  |
| GenCore version 5.1.6<br>ight (c) 1993 - 2005 Compugen Ltd.<br>arch, using sw model                                                              | January 31, 2005, 20:58:18; Search time 1845 Seconds (without alignments) 3152.647 Million cell updates/sec US-10-057-813-13_COPY_253_375 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 4526729 segs, 23644849745 residues of hits satisfying chosen parameters: 2299606     | ength: 0<br>ength: 123<br>Minimum Match                                                                 |   | 65         |                        |                                                                            | 9: 9b pr:*<br>10: 9b ro:*<br>11: 9b sts:*<br>12: 9b sy:*                                                         | 14: gb_vi:*                                                                          | No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, i derived by analysis of the total score distribution. | .*<br>Query<br>Match Length DB ID                                                      | 21.0 97 6 CQ461900 CQ | 19.0 89 4 AJ629187 AJ629187 S70266 TAP | 19.0 101 9 S70274S1 S70274 TA 19.0 101 9 HSITGAD02 U40275 HU 18.7 89 6 AX899550 AX899550 | 18.7 12.1 6 AX262947 AX262946 Sequent 18.7 12.1 6 AX262947 AX262947 AX262947 Sequent 18.4 90 6 A69898 Sequence 18.4 90 6 A | 2 18.0 17 6 CO665784 CO665787 P. 10.0 9 S7025651 S70256 TS 17.6 75 10 S60901 |
| nucleic -                                                                                                                                        | Kun on:<br>Title:<br>Perfect goore:                                                                                                       | table                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Searched:<br>Total number o                                                          | Minimum DB seq l<br>Maximum DB seq l<br>Post-processing:                                                | ı | Database : |                        |                                                                            |                                                                                                                  |                                                                                      | Pred. No.<br>score gree<br>and is de                                                                                                                                              | Result<br>No. Score                                                                    | c 1 25.8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 4.7.                                   | 2 6                                                                                      | 10<br>11<br>12<br>22                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 110<br>110<br>110<br>110<br>110<br>110<br>110<br>110<br>110<br>110                                                                                                              |

61

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S70266
TAP1 (TAP1-B) {ATP binding region} [human, Caucasoids, mRNA Partial, 100 nt].
Partial, 100 nt].
S770266
S770266.1 GI:546540
 AJ629187
Sus scrofa partial NFYA gene for nuclear transcription factor Y
 Submitted (27-FEB-2004) Barbosa A., Animal Genetic, Institut
National de Recherche Agronom., LREG, INRA/CEA, domaine de Vilvert,
78352 Jouy-en-Josas cedex, FRANCE
 29 CCCAGCCCTCCTCCTCAGACYCAGGGTCCAAGCCCCCCAACCCCTCCTTCCCCAGACC 88
 76 carreccieccácredragrercaccercacaciderrecrececrecredrefrenda 17
 Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
 44 CCTCACCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGG
 2 CCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGC
 A physical map of large segments of pig chromosome 7q1.1-q1.4: comparative analysis with human chromosome 6p21
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Barbosa, A.
 Submission
 39; Conservative
 74. .>89
 70
 89 CAGAGGTCC 97
 Unpublished
 62 TAGACCCC
 Similarity
 104 TGCTG 108
 16 rerre 12
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 Renard, C
 Direct
 1 pha
 Query Match
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Matches 39;
 VERSION
KEYWORDS
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ORGANISM
 RESULT 4
AJ629187/c
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S70266/c
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 BV185660 101 bp DNA linear STS 10-JUN-2004 squant48706 Human DNA (Sequenom) Homo sapiens STS genomic, sequence tagged site.
BV185660
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 Escherichia coli
Sebharichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
 5 AGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAG 64
 27 AGCTACTGCGCCTGCTGCGGCGACACACCTGCTGCTAATCGCTCTCCACAAAGGGCTAC 86
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Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Nelson, R.M., Marnellos, G., Kammerer, S., Hoyal, C.R., Shi, M.M., Cantor, C.R. and Braun, A.
Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
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 Length 100;
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3595 John Hopkins Court, San Diego, CA 92121,
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
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58.1%; Pred. No. 1.8e+04;
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Patent: EP 1260592-A 10334 27-NOV-2002;
 Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 101.
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Location/Qualifiers
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 Genome Res. (2004) In press
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Pharmaceuticals division
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 BV185660.1 GI:48024577
 19.3%;
58.0%;
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87 GCGCCGCAAAGTG 100
 65 ACCCCCTCACAGTG 78
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Best Local Similarity 58.0
Matches 40; Conservative
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AUTHORS
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101 bp DNA linear PRI 18-OCT-1996
Human beta-2 integrin alphaD subunit (ITGAD) gene, partial exon 16,
U40275
 41 CAGCCTCACCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGT 100
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1 (bases 1 to 10.1)

Wong, D. A., Davis E. M., LeBeau, M. and Springer, T. A.

Cloning and chromosomal localization of a novel gene-encoding a human beta 2-integrin alpha subunit
Gene 171 (2), 291-294 (1996)
 91 CAGTCCTGGGTGAGGTCCTGACCCCCACTAGGGCCTGTCCAAAATACTGCAGCCT 32
 Direct Submission
Submitted (07-NOV-1995) Dennis A. Wong, McMaster University,
Medicine, 1200 Main St. West, Hamilton, On L8N 3ZS, Canada
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|db_xref="GI:1173867"
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PUBMED
REFERENCE
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 TAPI (TAPI-C) {ATP binding and 3' regions} [human, Caucasoids, mRNA Bartial, 100 nt, segment 1 of 2].
S70274.1 GI:546541
 ö
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primatee; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 100)
Szafer,F., Oksenberg,J.R. and Steinman,L.
Immunogenetics 39 (5), 374 (1994)
 Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100)
22 Safer; F.; Oksenberg, J. R. and Steinman, L.
New allelic polymorphisms in TAP genes
Immunogenetics 39 (5), 374 (1994)
 GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 148273] from the original journal article.
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entry [NCBI gibbsq 148274] from the original journal article.
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PAT 26-OCT-2001
 PAT 26-OCT-2001
 60 GCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCTGGTGCTGCTCAGCCGGGA 119
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 10 CGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCC
 Gaps
 Kmiec,E.B., Gamper,H.B. and Rice,M.C.
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002A 337 04-OCT-2001;
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers
 Gaps
 Kmiec,E.B., Gamper,H.B. and Rice,M.C.
Targeted chromosomal genomic alterations with modified single
stranded oligonucleotides
Patent: WO 0173002-A 338 04-0CT-2001;
UNIVERSITY OF DELAWARE (US)
Location/Qualifiers
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 18.7%; Score 23; DB 6; Length 89; 60.3%; Pred. No. 4.8e+04; ive 0; Mismatches 25; Indels
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 linear
 DNA
 DNA
 AX262946 121 bp C
Sequence 337 from Patent WO0173002.
AX262946
 Sequence 338 from Patent WO0173002. AX262947
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 70 CTCACAGTGCGCCGCCATGTGCCTGCA 96
 sa recretererececedenterecentes 32
 AX262946.1 GI:16511745
 AX262947.1 GI:16511746
 Homo sapiens (human)
 Homo sapiens (human)
Query Match
Best Local Similarity 60.3
Matches 38; Conservative
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 Homo sapiens
 120 CCC 122
 10 GCC 8
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AX262947
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 PAT 18-DEC-2003
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 PAT 27-AUG-2002
 C12P21/02,C12P21/08,C12Q1/68//G06F17/30,C12N15/00,C12N5/00, PC
G06F15/40
 60 GCTAGACCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTGCTGCTCAGCCGGGA 119
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 Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases I to 89)
Edwards, J. B.D.M.; Duclair, E. and Jordan, J.Y.
Sequence tag and encoded human protein
Patent: JP 2001269182-A 11429 02-OCT-2001;
 Homo sapiens (human)
JP 2001269182-A/11429
02-OCT-2001
02-OCT-2000
D 2000118773
26-FEB-1999 US 60/122487
JEAN BAPUTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES
 Gaps
 ö
 Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y. Expressed sequence tags and encoded human proteins Patent: EP 1033401-A 15513 06-SEP-2000;
 linear
 Length 89;
 25; Indels
 linear
 Location/Qualifiers. Location/Qualifiers.
 Score 23; DB 6; I
Pred. No. 4.8e+04;
0; Mismatches 25;
 Sequence tag and encoded human protein. BD035183.1 GI:22576925 JP 2001269182-A/11429. Homo sapiens (human)
 Sequence 15513 from Patent EP1033401.
AX899650

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 INV 14-JAN-2003
 PAT 03-FEB-2004
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 39 CCCAGCCTCACCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGT 98
 86 CCGTGCCCCGTCTGCCCGAGGGCAGGATCCCCTCTTGTGTTGCTCGTGCCNAANTC 27
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1 (bases I to 106).

Ekbhetski, R., Cooper, R.L., Atwood, H.L. and Hampson, D.R. Expression profilling of mRNA obtained from single identified crustacean motor neurons: determination of specificity of
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 Query Match
18.0%; Score 22.2; DB 6; Length 117;
Best Local Similarity 54.2%; Pred. No. 7.9e+04;
Matches 39; Conservative 0; Mismatches 33; Indels
 th 18.4%; Score 22.6; DB 6; Length 90; Similarity 68.9%; Pred. No. 6.3e+04; 31; Conservative 0; Mismatches 14; Indels
 Liew,C.C., Marshall,W.E. and Zhang,H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 10710 12-SEP-2002;
Chondrogene Inc. (CA)
 linear
 90 CCAAGCTTGCATGCCTGCAGAACGCCGACAGCTCGTTCCCGGGGCT 46
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 2 CCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCT
 106 bp mRNA
P.clarkii mRNA; ac rich region (ID 2D).
254253
Z54253.1 GI:1001894
 Procambarus clarkii (red swamp crayfish)
Procambarus clarkii
 CQ665784 117 bp DNA Sequence 10710 from Patent WO02070737. CQ665784
 Invert. Neurosci. 1 (4), 341-349 (1996)
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 99 GTGGGTGCTGCT 110
 26 TŤTGGATČCNČŤ 15
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 Homo sapiens
 98039421
9372152
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Matches 3
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 Bource
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VERSION
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 JOURNAL
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 BD022719 90 bp RNA linear PAT 27-AUG-2002 Mirror plane symmetry selection and evolution of nucleic acid. BD022719
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 PAT 07-MAY-1999
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 63
 10 CGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCC
 4 cécriragiecrecériéséséséséresresresreséreséresérerresessasarrerer
 Gaps
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 1 (bases 1 to 90)
Bald, R., Erdmann, V.A. and Fuerste, J.P.
Bald, R., Erdmann, V.A. and Fuerste, J.P.
Bald, R., WO 9808856-A 27 05-MAR-1998;
BALD ROLF (DE)
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 Length 90;
 Length 121;
 46
 90 ccaadctrocarectrocadaacecceacaecretroceeeer 46
 40; Indels
 14; Indels
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 Match 18.4%; Score 22.6; DB 6; Local Similarity 68.9%; Pred. No. 6.3e+04; les 31; Conservative 0; Mismatches 14;
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Sequence 27 from Patent W09808856.

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 64 TCCTCTGTGCGCCGGTCTCTCCCCAGGA 90
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 BD022719.1 GI:22563942
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Best Local Similarity 54.0%;
Matches 47; Conservative
 A69898
A69898.1 GI:4774410
 JP 2001504448-A/27.
Homo sapiens (human)
Homo sapiens
 unidentified
unclassified
 unidentified
 Query Match
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ACCESSION
VERSION
 LOCUS
 ORGANISM
 BD022719/c
 ORGANISM
 Best Loc
Matches
 RESULT 12
A69898/c
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JOURNAL
 TITLE
JOURNAL
 ACCESSION
 REFERENCE
 AUTHORS
 VERSION
KEYWORDS
SOURCE
 AUTHORS
 KEYWORDS
SOURCE
 RESULT 13
 REFERENCE
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Location/Qualifiers

1. .106

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clone only partially sequenced (region proximal to the T7
primer)"
 19 CAGACTGAGGACAGCTGGGTCCCAGCCTCACAGAGGCTAGACCCCCTCACAGTG 78
 Pekhletski, R., Cooper, R.L., Hampson, D.R. and Atwood, H.L.
Expression profiling of mRNA obtained from single identified
crustacean motor neurons: determination of specificity of
hybridization
Unpublished
3 (bases 1 to 106)
Pekhletski, R.
Direct Submission
Submitted (28-SEP-1995) Pekhletski R., University of Toronto,
MSS 282
 0; Gaps
 Query Match 17.9%; Score 22; DB 3; Length 106; Best Local Similarity 55.1%; Pred. No. 9.2e+04; Matches 43; Conservative 0; Mismatches 35; Indels
 Search completed: January 31, 2005, 21:43:20 Job time : 1848 secs
 79 CGCCGCCATGTGCCTGCA 96
 64 CAACACCAGTACCACCA 81
 misc_feature
 source
 JOURNAL
REFERENCE
AUTHORS
TITLE
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| 18.2         123         2         BE171397         RC1-HT054           18.0         79         6         CB289729         CC1302865         PO15B0B         GC1302865         PO15B0B         GC1302865         PO15B0B         GC1302865         PO15B0B         GC1869072         CC1869072         CC186509         DNX449         Ba           18.0         102         4         BIO46042         RC1866072         RC1866072         RC1866072         RC1866024         RC1866024         Ba         Ba         Ba         CC1866024         Ba         Ba         Ba         Ba         CC186606         Ba         Ba         CG86906         Ba | ALIGNMENTS                                                                              | AA430669  AA430669  IMAGE: 770405 3', mRNA sequence.  NA430669  AA430669. GI:2111242  BA430669. GI:2111242  SA430669. GI:2111242  BOT BA43069. GI:2111242  BOT BA53069. GI:2111242  BOT BA5306. GI:21124124  BOT BA5306. GI:2111242  BOT BA5306. GI:2111242  BOT BA5306. GI:2111242  BOT BA5306. GI:21124  BO | sherry, maretacon, ratespon, r. and wilbon, r. sherry, EST Project 1997, published (1997) nitact: Wilson RK shington University School of Medicine 44 Porest Park Parkway, Box 8501, St. Louis, MO 63108 | Tel: 314 286 1800  Fax: 314 286 1810  Fax: 314 286 1810  Email: estGwatEon.wustl.edu  This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@mage.llnl.gov) for further information.  Possible reversed clone: polyr not found  Seq primer: -41m13 fwd. ET from Amersham  High quality sequence stop: 65.  High quality sequence stop: 65.  I97  /organism="Homo sapiens"  /mol type="mRNM"  /mol type="mRNM"  /db_xref="taxon:9606"  /clone="IMAGE:770405"  /clone="IMAGE:770405"  /clone="Thype="covarian tumor"  /lab_host="mange"  /clone="IMAGE:770405"  /clone="IMAGE:770405"  /clone="Lb="Soars ovary tumor NbHOT"  /note="Organ: ovary; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site=! Not !: Site=: Eco RI; lst strand cDNA was primed with a Not ! - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGCGGGTTTTTTTTTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
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| 25<br>26<br>27<br>26<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27<br>27                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | RESULT 1                                                                                | LOCUS DEFINITION ZW2 ACCESSION AA4 VERSION AA4 VERSION AA4 KEYWORDS EST SOURCE HOM ORGANISM HOM MAM REFERENCE 1 AUTHORS H1 AUTHORS H1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | TITLE WA<br>JOURNAL UN<br>COMMENT CC                                                                                                                                                                     | TE PROTURES High Post Se Se Source High Post Se Source High Post Section 1997 Secti |
| S.1.6 Compugen Ltd. Search time 1963 Seconds without alignments) 283.284 Million cell updates/sec 5tgctgctcagccgggacccc 123 esidues esidues                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |                                                                                         | cted by chance to have a                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | Description                                                                                                                                                                                              | AA430669 ZW26d03.8 BF171548 PCL2912 M BY074656 BY074656 AV631484 AV631484 AA092420 119365.8e AZ883677 RPCI-23-1 BX54226 Loishmani AI267761 QK06e12.x BQ972671 QHD4a07.y AA079036 Zm94h12.r N56039 J6239F Huma CC374455 PUHDW06TD BJ50478794 BJ472794 BG165373 QV1-H7047 BJ50478794 BJ472794 CC665407 CGCAH39TV BF291718 WHE2205 B CG708991 1119015C1 CC86444 SALK 1486 AI208489 QG55G04.x AZ62277 IM0482D12 CB435325 615414 MA BM312764 ig78g08.y BF956593 PM1-NN120                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compuge nucleic search, using sw model January 31, 2005, 20:59:38; search (without 2283.284 US-10-057-813-13_COPY_253_375 1 accaagctacgttccttcatgct indept 10.0, Gapext 1.0 32822875 seqs, 18219865908 residues of hits satisfying chosen parameters:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | length: 0 length: 123 3: Minimum Match 0% Maximum Match 100% Listing first 45 summaries | EST:*  'gb_estl:* 'gb_btc:* 'gb_estl:* 'gb_estl:* 'gb_estl:* 'gb_estl:* 'gb_estl:* 'gb_estl:* 'gb_estl:* 'gb_gssl:* 'gb_gssl:* 'gb_gssl:* 'gb_gssl:* 'gb_gssl:*                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | SUMMARIES                                                                                                                                                                                                | 21.0 97 1 AA430669 20.5 118 5 9171548 20.2 120 117 2 BF171548 20.2 120 1 14 AA032420 19.8 112 8 AZ883677 19.7 115 9 LBAP642F12 19.5 52 1 AA032420 19.5 122 5 BO972671 19.5 122 5 BO972671 18.9 116 8 CC374455 18.9 116 8 CC374455 18.9 117 4 BA57373 18.7 117 4 BA57373 18.7 117 2 BF291718 18.4 112 9 CC686444 18.2 115 9 CC686444 18.2 115 9 CC686444 18.2 122 9 CC886444 18.2 122 9 CC886444 18.2 122 4 BM312764 18.2 122 4 BM312764                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
| OM nucleic - nuc<br>Run on:<br>Title:<br>Perfect score:<br>Sequence:<br>Scoring table:<br>Searched:<br>Total number of                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | Minimum DB seg l<br>Maximum DB seg lo<br>Post-processing:                               | Database : 1 2 2 2 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  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/tissume_type="Blood"
//cell_type="Blood"
//dev_Eage="Blood"
//dev_Eage="Blood"
//dev_Eage="Blood"
//dov_Eage="Bloom cell leukemia"
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Xhoi; mRNA was purified from plasma cell leukemia
patient's peripheral blood containing >95% myeloma. An
oligo d(T)18 primer containing XhoI restriction site was
used to prime first strand synthesis using M-MLV reverse
transcriptase. To protect the cDNAs from XhoI digestion in
subsequent cloning step, the nucleotide analogue
5-methyl-dcTP was added to the nucleotide mixture and
[a-32P]dATP was added to monitor the quantity and
[a-32P]dATP was added to monitor the quantity and
and blunting of cDNA termini, EcoRI adapters were
ligated, followed by kinase treatment and digestion with
XhoI. The cDNAs were then size-fractionated using
Sephacryl S-500 column and then ligated into EcoRI and
 ö
 BF171548 117 bp mRNA linear EST 23-MAR-2001 PCL2912 Myeloma (PCL) cDNA library Homo sapiens cDNA, mRNA
 39 CCCAGCCTCACCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGT 98
 Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 117)
1 (Dases 1 to 117)
 Claddo,J.O., Masih.Khan,E., Tang,H., Goncalves,J., Voralia,M.,
Li,Z.H., Nadeem,V., Cukerman,E., Franciso-Pabalan,O., Liew,C.C.,
Woodgett,J.R. and Stewart,A.K.
A molecular compendium of genes expressed in multiple myeloma
the Not I and Eco RI sites of a modified pT/T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "
 Gaps
 University Health Network
610 University Ave., 5-126, Toronto, Ontario, M5G 2M9, Canada
Tel: (416) 946-4639
Fax: (416) 946-4546
Email: k.stewart@utoronto.ca
 ;
 Length 97;
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 BACKWARD: 5'-CCAGTGAATTGTAATACGACTCACTATAGGGCG-3'
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Location/Qualifiers
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 Contact: A. Keith Stewart, M.D. Oncology Research
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KEYWORDS
SOURCE
ORGANISM
 source
 BF171548/c
 DEFINITION
 TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
 ACCESSION
 AUTHORS
 REFERENCE
 RESULT 2
 FEATURES
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Mammalia, Eucheria; Rodentia; Sciurognathi; Muridae; Murinae; Murinae; Mammalia; Eucheria; Rodentia; Sciurognathi; Muridae; Murinae; Mikaido, I., Osato, M., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldaralli, R., Hill, D.P., Bult, C., Hume, D.A., Ouackenbush, J., Schrimi, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Godzik, A., Gough, J., Grimmond, S., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gariboldi, M., Hirokawa, N., Lenhard, B., L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., L., Majlott, D.B., Kawaji, H., Kawasawa, Y., Kediierski, R., Mill, H., Nagashima, T., Multais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pevan, W.J., Pertea, G., Pescolo, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Wagner, L., Walner, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Yangi, L., Yang, Z., Zavolan, M., S., Tagadale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Itch, M., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, T., Pukuda, S., Hara, A., Hashizume, W., Incean, Y., Lander, B., Rogers, J., Birney, B., Asakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Wataka, Y., Bataki, Y., Yanguishi, A., Sokai, K., Sasaki, D., Shibata, K., Shinayishi of the mouse transcriptome based on functional annotation of 60,770 full-length cDNa
 BY074656
BY074656 RIKEN full-length enriched, 16 days embryo heart Mus mussulus cDNA clone 1920096L06 5', mRNA sèquence.
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 extract.
 Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
1-81: 81-45-503-922
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 XhoI digested Lambda Zap Express vector. The ligation product was packaged using Gigapack II packaging extra The library had primary titre of approx. 1x106. Clones from the primary library were randomly selected for
 11 GITTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCCC
 Gapa
 .
0
 Length 117;
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Best Local Similarity 56.5%; Pred. No. 4.8e+03;
Matches 48; Conservative 0; Mismatches 37; Indels
 single pass sequencing."
 71 TCACAGTGCGCCGCCATGTGCCTGC 95
 41 rececececececaeracrecree 17
 Contact: Yoshihide Hayashizaki
 Mus musculus (house mouse)
Mus musculus
 BY074656.1 GI:26176407
 LOCUS
DEFINITION
 SOURCE
 RESULT 3
BY074656/c
 MEDLINE
PUBMED
COMMENT
 ACCESSION
 REFERENCE
 AUTHORS
 VERSION
KEYWORDS
 JOURNAL
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XhoI; The CDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
dioxide concentration in the bubbling gas was changed from
5% to 0.04%"
 119365.cq.F Human fetal heart, Lambda ZAP Express Homo sapiens AA092420
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/clone lib="Human fetal hearts is left."
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/khoi; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT weeks). cpriner. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."
 29 ACGCGGATACGCATTGTTGACACGCGCGCGCGTTGAACCGAGGCGCCCCCGACTTGAAGG 88
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 8 TACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACC 67
 1 ACCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGG
 Gaps
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 Length 120;
 42; Indels
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Location/Qualifiers
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BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG
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 61 CTAGACCCCTCACAGTGCGCCGCCATGTGCC 92
 75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
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 Email: cliew@rics.bwh.harvard.edu
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50; Conservative
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 (bases 1 to 114)
 Best Local Similarity 61.9
Matches 39; Conservative
 Unpublished (1996)
 .114
 Contact: Liew CC
 Fax: 6179750995
 Homo sapiens
 Best Local Similarity
 Liew, C.O
 ٠.
 Query Match
 Match
 SOURCE
ORGANISM
 DEFINITION
 TITLE
JOURNAL
COMMENT
 Matches
 ACCESSION
 REFERENCE
 AUTHORS
 RESULT 5
 VERSION
KEYWORDS
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 Query
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 AV631484 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas reinhardtii 5% to 0.04% CO2 Chlamydomonas reinhardtii cDNA clone LCL094g09_r 5', mRNA sequence.
 Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
 ö
 Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
 Asamizu, E., Mura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K., Nakamura, Y. and Tabata, S. Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
 Chlamydomonas reinhardtii
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission

Computational Analysis of Full-Length Mouse CDNAs Compared with
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 prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
 Gaps
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 CCAAGCAGCCGCAGCCTGAGGACCGCTCGGTCCCAGCCGC 27
 2 CCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTC 47
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 Location/Qualifiers
 Chlamydomonas reinhardtii
 AV631484
AV631484.1 GI:10794118
 20.5%;
 (bases 1 to 120)
 Conservative
 1. .118
 Query Match
Best Local Similarity
 11089912
 33;
 SOURCE
ORGANISM
 DEFINITION
 MEDLINE
PUBMED
 Matches
 ACCESSION
 VERSION
KEYWORDS
 REFERENCE
 AUTHORS
 JOURNAL
 FEATURES
 RESULT 4
 AV631484
 FEATURES
 TITLE
 COMMENT
 ORIGIN
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Email: capbs-remain.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
 Al262761 S2 bp mRNA linear EST 13-NOV-1998 qk06e12.xl NCI_CGAP_Kid3 Homo sapiens cDNA clone IMAGE:1868206 3' similar to SW:PRP4_HUMAN P10163 SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR; contains PTR5.b3 MSR1 repetitive element; , mRNA
 Eukaryoutai Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 52)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Gaps
 Leishmania braziliensis GSS, clone LBAF042F12, genomic survey
 Sao Paulo,
 Direct Submission
Submitted (17-UNN-2003) Cruz A.K., University of Sao Paul
Department of Molecular and Cell Biology, FMRP, Avenida
Bandeirantes 3900, Ribeirao Preto, SP, 14049-900, BRAZIL
Clone requests: akcruz@fmrp.usp.br.
 Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Leishmania; Leishmania braziliensis species complex.
 ö
 Length 115;
 71 derahadecerreadecrecededacachecrecereradadere
 Laurentino, E.C., Ruiz, J.C. and Cruz, A.K. GSS analysis of the Leishmania braziliensis genome Unpublished
 Score 24.2; DB 9; Length 1:
Pred. No. 1.4e+04;
0; Mismatches 13; Indels
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 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
 Trace considered overall poor
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High quality sequence stop: 1.
Location/Qualifiers
 GSS; genomic survey sequence.
Leishmania braziliensis
 Location/Qualifiers
 Leishmania braziliensis
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 19.7%;
71.1%;
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 (bases 1 to 115)
 32; Conservative
 sequence.
BX545265
BX545265.1
 Homo sapiens
 Query Match
Best Local Similarity
 Cruz, A.K
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 source
 LOCUS
DEFINITION
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SOURCE
ORGANISM
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 DEFINITION
 ORGANISM
 AUTHORS
TITLE
JOURNAL
 REFERENCE
AUTHORS
TITLE
JOURNAL
 ACCESSION
VERSION
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 VERSION
KEYWORDS
 REFERENCE
 RESULT 8
AI262761
 JOURNAL
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 FEATURES
 COMMENT
 TITLE
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 SOURCE
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E. (Dasses 1 to 112)
S. Abinret; B., Incilia, M., Megann, S., Teegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Squences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-187D12.TV
Contect: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Email: szhaoœtigr.org
 /Boch : was a part of the light GSS 05-MAR-2001
 ö
 GSS 23-JUN-2003
 end
Email: szkadetigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pdejongemail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC e
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 187 row: D column: 12
Seg primer: SP6
Class: BAC ends.
 Gaps
 ö
 68
 61
 19.8%; Score 24.4; DB 8; Length 112; 68.0%; Pred. No. 1.2e+04; ive 0; Mismatches 16; Indels (
 AZ883677 112 bp DNA linear G
RPCI-23-187D12.TJ RPCI-23 Mus musculus genomic clone
RPCI-23-187D12, genomic survey sequence.
 19 CAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCC
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Matches 34; Conservative
 LBAF042F12
 107 ACC 109
 68 CCC 70
 AZ883677
 110
 RESULT 6
AZ883677/c
 волисе
 RESULT 7
LBAF042F12
LOCUS
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Tel: 314 286 1810

Fax: 314 286 1810

Email: estGowatson.wustl.edu

WARNING: There is evidence that suggests that the 384-well parent
MARNING: There is evidence to that suggests that the selvent clones.

Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.
 AA079036 10 BT 23-DEC-1997 2m94h12.rl Stratagene colon HT29 (#937221) Homo sapiens cDNA clone IMAGE:545639 5' similar to gb:X17206 40S RIBOSOMAL PROTEIN S4
size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_IISB=Chemical induction TAG_LIB=OH_ABCDI sunflower RHABO1
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 90)
11 (lases 1 to 90)
11 (lases 1 to 90)
12 (chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hulkman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Passons, J., Prange, C., Rikfin, L., Rohlfing, T., Schallenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
 28 GACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCCCTCACAGAGTGCGCGCCGCAT 87
 85 GAATGCATCCTCCCAGAGGCGCCTGACTCCAGCCTAGCCACCCAAACCGTGGTCCGGCAC 26
 Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Trace considered overall poor quality Insert Length: 1017 Std Error: 0.00 Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 1.
 Gарв
 ö
 Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 19.5%; Score 24; DB 5; Length 122; larity 60.9%; Pred. No. 1.6e+04; Conservative 0; Mismatches 25; Indels
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 (HUMAN);, mRNA sequence.
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 Contact: Wilson RK
 Нощо варіепв
 and Marra, M.
 Similarity
 88 GTGC 91
 25 AGGC 22
 97044478
 8889549
 Query Match
 Local
 source
 RESULT 10
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KEYWORDS
SOURCE
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 Officer, yg.abl QH ABCDI sunflower RHA801 Helianthus annuus CDNA Clone QHD4a07, mRNA sequence.
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 Helianthus annue Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Asteroideae; Helianthus asterids; Asteroideae; Helianthus asterids; Asteroideae; Mathoneae; Helianthus asterids; Asteroideae; Losza, Machelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Lin, H., van Damme, M., Lavelle, D., Chevaller, P., Ziegle, J., Blison, P., Kolkman, J., Slabudy, M.S., Livingston, K., Zhou, Y., Lei, Z., Church, S., Jackson, L. and Bradford, K.
 /tobe="Organ: Kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; lst strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. mRNA source: 2 pooled kidneys. Library went through one round of normalization. Library constructed by Bento Soares and M. Fatima Bonaldo.
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 Gaps
 ö
 Contact: Accarder Kozik [R.W.Michelmore]
Contact: Accarder Kozik [R.W.Michelmore Lab
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
Singleton, see http://cgpdb.ucdavis.edu/ for details.
Plate: QHD4 row: a column: 07.
Location/Qualifiers
 49
 29 ACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCCCTCACAG 76
 ACAGCGCGCGCCCTCCTGCCCCCACAAAGGGGGGAGACCCCCCCGCGG
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 JOURNAL
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 VERSION
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SOURCE
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 AUTHORS
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 TITLE
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Oryzias latipes (Japanese medaka)
Oryzias latipes
 Location/Qualifiers
 Email: whitelaw@tigr.org
 Unpublished (2003)
Other GSSs: PUHDW06TB
Contact: Cathy Whitelaw
 genomic survey sequence
 GI:30848072
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 ends
 Tel: 301-838-5843
Fax: 301-838-0208
 Seg primer: TF
Class: sheared
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BJ504782
 67 CCCCTCAC 74
 48 CTCCACGC 41
 ČC374455
CC374455.1
 Query Match
Best Local Similarity
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BJ504782
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 N56039 110 bp mRNA linear EST 20-FEB-1996 J6239F Human fetal heart, Lambda ZAP Express Homo sapiens CDNA clone J6239 5', mRNA sequence.
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 CC374455 116 bp DNA linear GSS 19-MAY-2003 PUHDW06TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa429All,
XhoI; Cloned unidirectionally. Primer: Oligo dr. From adenocarcinoma HT-29 (HTB 38), modezately differentiated grade II. Average insert size: 1.5 kb; Uni-ZAP XR Vector; 5' adaptor sequence: 5' GAATTCGGCACGGG 3' ~3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTT 3'"
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Xho1; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoR1 adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."
 29 ACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCCCTCACAGTGCGCCCATG 88
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 110)
 64 ACCGCTGTTCCCCATCCCANGCCAACNCAGGCCCCGGCCCCNNGCTGTACCNTGTCATC 5
 83
 25
 0; Gaps
 110 AACTGGGGCCTGCCCTCTGCAGCCACAGTGGGGGCCCCCACAGTGGGGCGTCCATGT
 31 AGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGT
 Gaps
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 Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
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 Fax: 6179750995
Email: cliew@rics.bwh.harvard.edu
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Location/Qualifiers
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Contact: Liew CC
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 N56039.1 GI:1198887
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Homo sapiens
 Query Match
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Matches 37; Conservative
 1. .110
 89 TGCC 92
 Liew, C.C.
 4 CGCC 1
 RESULT 12
CC374455/c
LOCUS
 DEFINITION
 DEFINITION
 ORGANISM
 RESULT 11
N56039/c
 REFERENCE
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BJSO4782
BJSO4782 MF01FSA CDNA Oryzias latipes CDNA clone MF01FSA011P06 3',
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoldeae, Andropogoneae, Zea.
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 99
 49
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 7 CTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGAC
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Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
Maize Genomics Consortium
 ö
 Length 116;
 9712 Medical Center Drive, Rockville, MD 20850, USA
 ch 18.9%; Score 23.2; DB 8; Length 1. Similarity 58.8%; Pred. No. 2.8e+04; 40; Conservative 0; Mismatches 28; Indels
 Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Fax: 81-559-81-6855
```

Gape

6

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Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Fooideae; Triticeae; Hordeum.

E. (bases 1 to 117)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact Tadasu Shin-i
Contact Tadasu Shin-i
Contact Tadasu Shin-i
Contact Fox Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
 BJ472794 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA BJ472794 K. BJ472794 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA BJ472794
 tissue mRNA and cDNA amplification were performed under low stringency conditions."
 1 ACCAAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCCAGCCTCACCTGACACAGGG
 35 GGGTCCCAGCCTCACCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTG
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 87
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 52 ccecreerercrecrecrecentes 26
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/cultivar="Haruna Nijo"
 Email: tshini@genes.nig.ac.jp.
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 61 CTAGACCCCTCACAGTGCGCCGCCAT
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Matches 47; Conservative
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SOURCE
ORGANISM
 RESULT 15
BJ472794/c
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 112)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Goldman, G.H., Carvalho, A.F., Magai, M.A., Ga Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
 Tel: +55-11-2704922

Fax: +55-11-2707001

Bmail: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=QV1-HT0474-070
300-097-hlist3=2000-03-07&44=1)

Seq primer: puc 18 forward

High quality sequence start: 9

High quality sequence stop: 113.
 ö
 BE165373 11.JUN-2000 2V1-HT0474-070300-097-h11 HT0474 Homo sapiens cDNA, mRNA sequence.
 Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Shotgun sequencing of the human transcriptome with ORF expressed
 Gaps
 86
 45 CTCACCTGACACAGGGCTAGACCCCCTCACAGTGCGCCCCATGTGCCTGCAGT
 CTCCTTNAATAANGCCTTGCCGCCCTCATCGCGCGCAATCTTGCGCCAGCAGT
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 sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Email: tshini@genes.nig.ac.jp.
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 BE165373.1 GI:8628094
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 BE165373
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 ACCESSION
VERSION
KEYWORDS
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AUTHORS
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Adp05517 Novel mic Acd70591 E. coli K Adk91981 Polynucle Adc35401 PCR prime Abn59212 Human spl Acd72441 E. coli K Acd8549 Human gen Acd8549 Human gen Ach8549 Human gen

Abn54356 Mouse spl

Adk91466 Polynucle Ad180566 Human rec Abn57458 Mouse spl Aac20910 Human sec Adm96137 Rat antis Aba69447 Human foo Ak43526 Human gen Aba17656 Human gen Ab17656 Human gen Adh92553 Human gen Adh35911 Human gen

score:

Title: Perfect

Sequence:

Minimum DB Maximum DB

Database

Searched:

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and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polymucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II) or antigen presenting cells that express (II). (I) has cytostatic detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological
 The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour
 Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing
 Human; ovarian cancer; ovarian tumour; cytostatic; gene;
 Human ovarian cancer related cDNA clone SEQ ID NO:4678.
 ALIGNMENTS
 Claim 1; SEQ ID NO 4678; 489pp; English.
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ADM96137
AAI24307
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AAH34256
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ABN59043
 ADK91466
 ADH92553
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 ADK91981
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 26-MAY-2000; 2000US-0207484P
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 Algate PA, Harlocker
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 (CORI-) CORIXA CORP.
 WO200192581-A2.
 Homo sapiens.
 06-DEC-2001.
 polypeptide
ABL81700;
 RESULT
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 Ab181700 Human ova
Adf86506 Single nu
Adc40305 Human sec
Adc40305 Human sec
Aba77422 p53 mutat
Aba77421 p53 mutat
Aba77430 p53 mutat
Adc7040 Human imm
Adc70404 Human imm
Adc70397 Human imm
Adc7014 E. coli K
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Ach1139 Human sec
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Ad180264 Human rec
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Acc173057 E. coli K
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 January 31, 2005, 20:17:18; Search time 269 Seconds (without alignments) 2400.293 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 Description
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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 US-10-057-813-13_COPY_253_375
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 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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ADC40305
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ABA77492
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ADF87025
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AAK70397
ADF87024
ACD76144
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geneseqn2003as:*
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Match
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 Scoring table:
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Result 8

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Sequence 121 BP; 18 A; 47 C; 31 G; 24 T; 0 U; 1 Other;

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hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polymucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is tumed for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA
 of polymucleotide
 Sequence 97 BP; 15 A; 18 C; 53 G; 11 T; 0 U; 0 Other;
detecting
 library using well known techniques
8888888888888888
```

Gaps ö Score 25.8; DB 6; Length 97; Pred. No. 1.9e+02; 0; Mismatches 37; Indels 99 GTGGGTGCTGCTCAGCCGGGACCCC 123 37 ACCTCCGCTGCCTCGGCGCGACCCC 13 21.0%; 56.5%; 48; Conservative Local Similarity Query Match Matches ò 유 ò 셤

ô 86

> Single nucleotide polymorphism detection human gene, SEQ ID No 89. ADF86506 standard; DNA; 121 BP. 26-FEB-2004 (first entry) ADF86506; ADF86506 \$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\frac{1}{2}\$\$\fra

human; single nucleotide polymorphism; microarray; side effect; gene; ds. Homo sapiens

JP2003235571-A.

26-AUG-2003

12-FEB-2002; 2002JP-00034717.

12-FEB-2002; 2002JP-00034717.

(KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

Novel polynucleotide useful for detecting single nucleotide polymorphisms in human gene.

Claim 1; SEQ ID NO 89; 704pp; Japanese.

The invention relates to a novel polymucleotide isolated and purified from a human gene having any one of 915 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligomucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1220 fully defined sequences as given in specification; a labelling probe containing the SNP containing oligo; and a microarray equipped with the SNP containing oligo. The isolated human gene of the invention is useful for detecting the single nucleotide polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide plumorphisms in a human gene. This polymucleolide sequence represents one of the 935 isolated polynucleotides from a human gene of the

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 Biochip containing probes complementary with open reading frames in Escherichia coli Kl2, useful for detecting gene expression and expression
 29 cridedriccicacaricricardadadedecerenciacicadeceadeadeceerriridea 88
 33 CTGGGTCCCAGCCTCACCTGACACAGGGTAGACCCCCTCACAGTGCGCCGCCATGTGCC
 Gape
 88.
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Score 25.2; DB 10; Length 121;
Pred. No. 3.1e+02;
 Biochip; gene expression; gut; diagnostic; detection; probe;
 39; Indels
 E. coli K12 MG1655 biochip probe SEQ ID 10334.
 1; Mismatches
 Weber J;
 93 TGCAGTGTGGTGCTGCTCAGCCGGGAC 120
 Huber A,
 ACD79058 standard; DNA; 100 BP
20.5%;
54.5%;
 17-MAY-2001; 2001EP-00112179.
 17-MAY-2001; 2001EP-00112179.
 (first entry)
 Best Local Similarity 54.5
Matches 48; Conservative
 Drescher B,
 (MWGB-) MWG-BIOTECH AG
 WPI; 2003-241155/24.
 Escherichia coli.
 19-SEP-2003
 EP1260592-A1
 27-NOV-2002.
 Donner H,
 ACD79058;
Query Match
 patterns.
 RESULT 3
 ACD79058
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Sequence 100 BP; 23 A; 37 C; 27 G; 13 T; 0 U; 0 Other;

in the invention

reactivity and reproducibility); also synthetic probes are generally shorter than probes prepared by polymerase chain reaction. ACD68731 to ACD81540 represent oligonucleotide probes used with the biochip described

This invention describes a novel biochip comprising probe spots, each containing many identical probes. The probes are nucleotide sequences of 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at least one includes a segment of at least 20 bases identical with, or complementary to, a segment of an open reading frame (orf) of Escherichia (orl K12. The blochip is used for specific detection of gene expression in K12 and for determining the gene expression pattern, e.g. for diagnostic determination of which E. coli strains are present in the gut, and to determination of which E. coli strains are present in the gut, and to determine the effects of e.g. growth media on gene expression. The blochip provides as comprehensive as possible detection of the K12. Conting provides as comprehensive of many different genes with a single genome, with simultaneous analysis of many different genes with a single cypric, and comparison of gene expression, it also allows measurements of population densities for the various strains. The use of synthetic oligonucleotides for preparation of probes allows free

Claim 3; Page 1611; 2004pp; German.

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Ashkenazi A, Botstein D, Desnoyers L, Eaton DL, Felloard A; Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A; Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ, Kljavin IJ; Marher JP, Pan J, Paoni NF, Roy MA, Stewart TA, Tumas D;
 Novel secreted and transmembrane polypeptides and polynucleotides
 26-UU-1999; 99US-0145698P.
28-UU-1999; 99US-0145622P.
28-UU-1999; 99WO-USC22594.
13-SEP-1999; 99WO-USC22594.
15-SEP-1999; 99WO-USC21090.
15-SEP-1999; 99WO-USC21090.
20-NOV-1999; 99WO-USC21313.
20-NOV-1999; 99WO-USC2813.
20-NOV-1999; 99WO-USC28564.
20-DEC-1999; 99WO-USC28564.
20-DEC-1999; 99WO-USC28564.
20-DEC-1999; 99WO-USC28565.
16-DEC-1999; 99WO-USC38099.
20-DEC-1999; 99WO-USC38565.
11-FEB-2000; 2000WO-USC31099.
21-FEB-2000; 2000WO-USC31099.
22-FEB-2000; 2000WO-USC31099.
22-MAR-2000; 2000WO-USC05641.
 970S-0063734P-
970S-0063734P-
970S-0064215P-
970S-0064248P-
970S-0064248P-
970S-0064248P-
970S-0065846P-
970S-0065846P-
970S-0065846P-
970S-0065846P-
970S-0065846P-
970S-0065846P-
970S-0065846P-
970S-0065846P-
970S-006645P-
970S-006645P-
970S-0066472P-
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970S-0066472P-
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970S-0066472P-
970S-0066472P-
 98WO-US019437.
98US-0104080P.
98US-0109304P.
98WO-US025108.
 98US-0100262P
 98WO-US019177
 98WO-US019330
98US-0100858P
 98US-0113296P
 99US-0143048P
99US-0145698P
 (GETH) GENENTECH INC.
 WPI; 2003-540676/51.
29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
29-OCT-1997;
31-OCT-1997;
31-OCT-1997;
31-OCT-1997;
31-OCT-1997;
12-NOV-1997;
12-NOV-1997;
24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
24-NOV-1997;
25-NOV-1997;
25-NOV-1997;
 04-JUN-1998;
10-SEP-1998;
10-SEP-1998;
14-SEP-1998;
 17-SEP-1998;
13-OCT-1998;
20-NOV-1998;
01-DEC-1998;
 14-SEP-1998;
16-SEP-1998;
17-SEP-1998;
 22-DEC-1998
07-JUL-1999
 27 AGCTACTGCGCCTGCTGCCGACACAGCCTGCTGCTATCGCTCTCCACAAGGGCTAC 86
 Human; PCR; primer; ss; PRO; secreted; transmembrane; therapeutic; tissue typing; immunohistochemical staining; gene therapy; neonatal heart; vascular endothelial growth factor; VEGF; proliferation; endothelial cell; stimulated T-lymphocyte; retinal neuron; rod photoreceptor cell; c-fos; glucose; FFA; chondrocyte; cardiac insufficiency disorder; wound; cancer; tumour; retinal disorder; retinitis pigmentosum; obesity; diabete; hyperinsulinaemia; hypoinsulinaemia; hypoinsulinaemia; one disorder; cartilage disorder; sport injury; arthritis; cardiant; vulnerary; cytostatic; ophthalmological; osteopathic; antiarthritic; anorectic.
 5 AGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAG 64
 Gaps
 .
0
 Length 100;
 31; Indels
 Human secreted/transmembrane protein, #52, PCR primer #3.
 Score 24.4; DB 8;
Pred. No. 5.4e+02;
0; Mismatches 31;
 ADC40305 standard; DNA; 118 BP.
 97US-0059113P

97US-0059113P

97US-0059111P

97US-0059121P

97US-0059122P

97US-0059128P

97US-0059268P

97US-0062287P

97US-0062287P

97US-0062287P

97US-0062814P

97US-0062814P

97US-0063120P

97US-0063120P

97US-0063124P

97US-0063124P

97US-0063124P

97US-0063124P

97US-0063124P

97US-0063544P

97US-0063544P

97US-0063544P

97US-0063544P

97US-006354P

97US-006354P

97US-006354P

97US-006354P

97US-006354P

97US-006354P

97US-006354P
 Query Match
Best Local Similarity 58.1%;
Matches 43; Conservative
 13-JUL-2001; 2001US-00905381
 GCCGCCCAAAGTG 100
 65 ACCCCCTCACAGIG 78
 18-DEC-2003 (first entry)
 US2003059829-A1.
 28-OCT-1997;
29-OCT-1997;
29-OCT-1997;
 24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
24-0CT-1997;
27-0CT-1997;
 Homo sapiens.
 -OCT-1997;
-OCT-1997;
-OCT-1997;
 5-OCT-1997;
 27-MAR-2003
 ADC40305;
 RESULT 4
ADC40305
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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

Homo sapiens, EP1033401-A2 06-SEP-2000.

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The invention discloses isolated PRO secreted/transmembrane polypeptides and the muclets caid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide for linking a bioactive molecule to a cell expressing a PRO polypeptide are useful for modulating and confecting other PRO polypeptides are useful for detecting other PRO polypeptides in a sample and for linking a bioactive molecule to a cell expressing a PRO polypeptides are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides or polypeptides are useful for modulating the biological activity of a cell expressing PRO polypeptides. The PRO polypeptides or polymetic and the processor or polymetic and are useful for stimulating hypertrophy of monatal heart, inhibiting vascular endothelial cells, modulating the proliferation of endothelial cells, modulating the proliferation of endothelial cells, modulating proliferation of endothelial cells, inducing proliferation of ethoracoves, enhancing the survival or proliferation of endothelial cells, modulating of software control or treating datoracoves. In particular, these are useful for ethoracoves or properties or proliferation of chondrocytes, inducing proliferation of chondrocytes, cup. Myperinal neurons or rod phocroceptor cells, inducing proliferation of chondrocytes, cup. Appendica, hypotimenial cells, modulating or bossity, diabetes, hypotimical profices are useful for ethoracoves or properties and their portions are useful in manmals. PRO polypeptides and their portions affect the expression of genes which have a role in cell death. The polymucleotides are useful in molecular biology including uses as hybridiation of entrempended or properties and properties of therapeutically useful research or properties and processed or combinantly expressing the protein and for the development and screening of therapeutic angents, for generating component and provesses as therapeutic gents of native processes of supplied a
 purification of PRO from recombinant cell culture or natural sources. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequence presented is a PCR primer which was used to
encoding them useful for treating skin, neurodegenerative diseases, as antithrombotic agent and for inducing endothelial cell apoptosis.
 SEQ ID NO 283; 473pp; English
```

diagnostic, forensic, gene therapy and chromosome mapping procedures

Claim 1; SEQ ID NO 15513; 71pp + Sequence Listing; English.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

Giordano J;

Duclert A,

Dumas Milne Edwards J, WPI; 2000-500381/45.

(GEST ) GENSET

21-FEB-2000; 2000EP-00200610

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RESULT 6
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 4 AAGCTACGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTA 63
 ..
0
 18.9%; Score 23.2; DB 10; Length 118;
llarity 53.3%; Pred. No. 1.3e+03;
Conservative 0; Mismatches 43; Indels 0.
 Indels
Sequence 118 BP; 25 A; 35 C; 35 G; 23 T; 0 U; 0 Other;
 83 GACCCATCACTGAGACTGCTGTGTGCCGGC 114
 95
 64 GACCCCTCACAGTGCGCCGCCATGTGCCTGC
 AAC11438 standard; cDNA; 89
 Query Match
Best Local Similarity
Matches 49; Conserv
 AAC11438;
```

Human secreted protein 5' EST, SEQ ID NO: 15513

(first entry)

06-OCT-2000

BXHXHXB

RESULT 5 AAC11438/c

g ò

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The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dr primed cDNA libraries. Such ESTs are not wall suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs and genomic DNAs. 5' ESTs are also used in
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 60 GCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTGCTGCTCAGCCGGGA 119
 70 GCTCGTCCGTCTCCGCGTGCGCCACCGCCGCCGCTACTGCTGCTGCTGCTCCTCCGGAT 11
 Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V; cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2; adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilia; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; ADCE; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR; familial hypercholesterolaemia; UGT1; syndrome; APP; PSBN1; antisense;
 diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
 Gape
 .
o
 Length 89;
 0; Mismatches 25; Indels
 p53 mutation correcting oligonuclectide SEQ ID NO: 338.
 Sequence 89 BP; 19 A; 24 C; 40 G; 6 T; 0 U; 0 Other;
 Score 23; DB 3;
Pred. No. 1.4e+03;
 expression and secretion vectors
 ABA77492 standard; DNA; 121 BP.
 18.7%;
60.3%;
 24-JAN-2002 (first entry)
 Query Match
Best Local Similarity 60.39
Matches 38; Conservative
 120 CCC 122
 10 GCC 8
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amplify a PRO polynucleotide of the invention.

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The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoblascoma, BRCAL, BRCAL, CFTR, CYCIN-dependent kinase inhibitor 2A (CDKMZA), APC, Pactor V, Factor VIII, Factor IX, haemoglobin alpha locus (HBA1), haemoglobin alpha locus 2 (HBA2), MLH1, MSH2, MSH6, application E (APOSS), LD receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor procein (APC), presentlin-1 (PSEN1) and presentlin-2 (PSEN2). These can be used in the gene therapy of diseases such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophilia, hypercholesterolaemia, thalassaemia, aickle cell anaemia, alzheimer's disease, melanoma, adenomatous polyposis of the colon and variance is sone of the gene correcting
 10 CGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCC 69
 cecriraciecrecericadecadericardadecrecerrirerrecedadarrerer 59
 adenomatous polyposis of the colon; Factor VII; Factor IX; thrombosis; haemophilis; alpha thalassaemia; haemoglobin alpha locus 1; MLH1; APOE; mismatch repair; MSH2; MSH6; hyperlipidaemia; apolipoprotein E; LDLR; familial hypercholesterolaemia; UGT1; syndrome; APP; PSEN1; antisense; UDP-glucuronosyltransferase; amyloid precursor protein; presentlin-1; Alzheimer's disease; cytostatic; antisickling; antisnaemic; haemostatic;
 cyclin-dependent kinase inhibitor 2A; CDKN2A; melanoma; APC; HBA1; HBA2;
 Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical
 Score 23; DB 4; Length 121; Pred. No. 1.5e+03;
 40; Indels
 Sequence 121 BP; 30 A; 31 C; 43 G; 17 T; 0 U; 0 Other;
 0; Mismatches
 70 CTCACAGTGCGCCGCCATGTGCCTGCA 96
 se recrerencececeerereceage 32
 various syndromes. The present secoligonucleotides of the invention
 Claim 7; Page 63; 294pp; English.
 Rice MC;
 ВР.
 27-MAR-2000; 2000US-0192176P.
27-MAR-2000; 2000US-0192179P.
01-JUN-2000; 2000US-0208538P.
30-OCT-2000; 2000US-0244989P.
 27-MAR-2001; 2001WO-US009761.
 18.7%;
54.0%;
 ADF87025 standard; DNA; 121
 26-FEB-2004 (first entry)
 47; Conservative
 Gamper HB,
 (UYDE) UNIV DELAWARE
 WPI; 2001-639230/73.
 Local Similarity
 antilipemic; ss
 WO200173002-A2.
 modification.
 Homo sapiens
 04-OCT-2001
 Kmiec EB,
 118
 ADF87025;
 Query Match
 Matches
 ADF87025/
 셤
 HXXXH
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 ઠે
 The present invention provides single-stranded oligonucleotides which can be used for the targeted alteration of genomic sequences, where the oligonucleotide has at least one mismatch compared with the genomic sequence to be altered. In particular, these sequences are directed at the following genes: adenosine deaminase, p53, beta-globin, retinoplastoma, BRCA1, BRCA2, CFTR, cyclin dependent kinase inhibitor 2A (CDENZA), APC, Factor V, Factor VII, Factor IX, haemoglobin alpha locus apolipoprotein B (APOR), LDL receptor (LDLR), UDP-glucuronosyltransferase (UGT1), amyloid precursor protein (APC), presentiin-1 (BSEN1) and presentilin-1 (B
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 céctitagracificacides de des de contra de la contra del contra de la contra del la contra del la contra del la contra de la contra del la contra de la contra de contra del la co
UDP-glucuronosyltransferase, amyloid precursor protein, presenilin-1, Alzheimer's disease, cytostatic, antisickling, antianaemic, haemostatic,
 Oligonucleotide for targeted alterations of genetic sequences and for treating cystic fibrosis, comprises at least one mismatch and chemical
 Human; gene therapy; adenosine deaminase deficiency; p53; beta-globin; retinoblastoma; BRCA1; BRCA2; CFTR; cystic fibrosis; cancer; Factor V;
 such as cancer, adenosine deaminase deficiency, cystic fibrosis, haemophila, hyperrolesterolaemia, thalassaemia, sickle cell anaemia, Alzheimer's disease, melanoma, adenomatous polyposis of the colon and various syndromes. The present sequence is one of the gene correcting
 CGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCC
 0; Gaps
 Length 121;
 40; Indels
 p53 mutation correcting oligonucleotide SEQ ID NO: 337.
 Sequence 121 BP; 17 A; 43 C; 31 G; 30 T; 0 U; 0 Other;
 Score 23; DB 4; Pred. No. 1.5e+03;
 0; Mismatches
 96
 90
 70 CTCACAGTGCGCCGCCATGTGCCTGCA
 64 recrererecececearereceaea
 oligonucleotides of the invention
 Claim 7; Page 63; 294pp; English.
 ABA77491 standard; DNA; 121 BP
 27-MAR-2000; 2000US-0192179P.
01-JUN-2000; 2000US-0208538P.
30-OCT-2000; 2000US-0244989P.
 27-MAR-2001; 2001WO-US009761.
 27-MAR-2000; 2000US-0192176P.
 18.7%;
 Best Local Similarity 54.0%;
Matches 47; Conservative
 (first entry)
 Kmiec EB, Gamper HB,
 (UYDE) UNIV DELAWARE
 WPI; 2001-639230/73.
 antilipemic; ss.
 WO200173002-A2.
 Homo sapiens
 modification
 24-JAN-2002
 10
 ABA77491;
 4
 Query Match
 ABA77491/
8
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 EEKEKEK
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Gape

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2000US-0190076P.
2000US-0198123P.
2000US-0205515P.
2000US-0209467P.
2000US-0214886P.
 2000US-0186350P.
2000US-0189874P.
 2000US-0180628P
 2000US-0218290P.
2000US-0220963P.
 2000US-0224518P
 2000US-0225214P
 2000US-0225270P.
 2000US-0231413P
 2000US-0237037P
 16-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
 14-AUG-2000
 02-OCT-2000;
 14-AUG-2000
14-AUG-2000
 14-SEP-2000
 14-AUG-2000
 14-AUG-2000
 .4-SEP-2000
 22-AUG-20
 The invention relates to a novel polymucleotide isolated and purified from a human gene having any one of 915 fully defined sequences as given in specification, or a sequence having a base substitution. The invention further relates to: an oligonucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1220 fully defined sequences as given in specification; a labelling probe containing the SNP containing oligo, and a microarray equipped with the SNP containing plago. The isolated human gene of the invention is useful for detecting the single nucleotide polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effective in detecting single nucleotide polymorphisms in a human gene. This polymucleotide sequence represents in a numan gene. This polymucleotide sequence represents in a numan gene of the suman gene of the
 ö
 Novel polynucleotide useful for detecting single nucleotide polymorphisms
 human; single nucleotide polymorphism; microarray; side effect; gene; ds.
 Gaps
 Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25212.
 Single nucleotide polymorphism detection human gene, SEQ ID No 608.
 ;
 Score 22.8; DB 10; Length 121;
Pred. No. 1.8e+03;
1; Mismatches 8; Indels 0;
 Sequence 121 BP; 23 A; 40 C; 43 G; 14 T; 0 U; 1 Other;
 64 GACCCCTCACAGTGCGCCCATGTGCCTGCAGTG 99
 61 KACCGCCTCACATTGCTCCACCAGGTGCCTGTGGGG 26
 Claim 1; SEQ ID NO 608; 704pp; Japanese
 (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
 12-FEB-2002; 2002JP-00034717.
 12-FEB-2002; 2002JP-00034717,
 Query Match 18.5%;
Best Local Similarity 75.0%;
Matches 27; Conservative
 WPI; 2003-820454/77
 JP2003235571-A.
 in human gene.
 Homo sapiens
 26-AUG-2003
 nvention
 RESULT 9
요
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid.gequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polynuclectides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
cupplement the patients own production of (I). Additionally, (I)
cupplement the patients own production of (I). Additionally, (I)
cupplement the patients own production of (I). Additionally, (I)
cupplement the patients own production of (I). Additionally, (I)
cupplement the patients own production of (I). Additionally, (I)
cupplement the patients own production of (I). Additionally, (I)
cancers and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54912 to AAK54950 and AAM82169
crepresent sequences used in the exemplification of the present invention
 14 TCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCCCTCA 73
 recerchéacheracernácererrechéacererechécerechéacerececerená
 Human, immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
 0; Gapa
 Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25209.
 18.4%; Score 22.6; DB 4; Length 121; 60.7%; Pred. No. 2.1e+03; ive 0; Mismatches 24; Indels (
 Sequence 121 BP; 34 A; 19 C; 56 G; 12 T; 0 U; 0 Other;
 31-JAN-2000; 2000US-0179065P.
24-FEB-2000; 2000US-018062BP.
02-MAR-2000; 2000US-0184664P.
02-MAR-2000; 2000US-018936P.
11-MAR-2000; 2000US-0189374P.
17-MAR-2000; 2000US-019812BP.
19-MAY-2000; 2000US-019812BP.
19-MAY-2000; 2000US-020551SP.
28-JUN-2000; 2000US-021886FP.
30-JUN-2000; 2000US-02181886P.
 AAK70397 standard; DNA; 121 BP.
 2000US-0217487P.
2000US-0217496P.
 2000US-0218290P
2000US-0220963P
 26-JUL-2000; 2000US-0220964P
 17-JAN-2001; 2001WO-US001354
 06-NOV-2001 (first entry)
 37; Conservative
 Best Local Similarity
 WO200157182-A2
 74 C 74
 Homo sapiens.
 09-AUG-2001
 AAK70397;
 Query Match
 65
 Matches
요
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 Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
 Disclosure; SEQ ID NO 25212; 3071pp + Sequence Listing; English.
 Ruben SM
 2000US - 0241221P

2000US - 0241785P

2000US - 0241787P

2000US - 0241809P

2000US - 0241826P

2000US - 0241817P

2000US - 0246474P

2000US - 0246476P

2000US - 0246476P

2000US - 0246476P

2000US - 0246476P

2000US - 0246524P

2000US - 0246521P

2000US - 0249211P

 (HUMA-) HUMAN GENOME SCI INC.
 Rosen CA, Barash SC,
 WPI; 2001-483426/52
 08-NOV-2000;
 08-NOV-2000;
 08-NOV-2000;
 08-NOV-2000;
 7-NOV-2000;
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2000US-0224519P.
2000US-0225213P.
2000US-0225214P.
2000US-025266P.
 2000US-0230438P
2000US-0231242P
2000US-0231243P
2000US-0231244P
 2000US-0232081P.
2000US-0231968P.
2000US-0232397P.
2000US-0232398P.
 2000US-0225267P.
2000US-0225268P.
2000US-0225270P.
 2000US-0231413P.
2000US-0231414P.
2000US-0232080P.
 2000US-0236369P
 2000US-0246476P
 14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
 06-SEP-2000;
 08-NOV-2000;
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08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246573P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246525P.
08-NOV-2000; 2000US-0246527P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-024651P.
08-NOV-2000; 2000US-024651P.
08-NOV-2000; 2000US-024651P.
08-NOV-2000; 2000US-024651P.
17-NOV-2000; 2000US-024651P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249208P.
 17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
 2000US-0249265P.
2000US-0249297P.
2000US-0249299P.
 2000US-0251030P.
 2000US-0251479P
 05-JAN-2001;
 17-NOV-2000
```

(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM,

WPI; 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 25209; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)

amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
proteins and polymucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
example, they may be used to treat disorders associated with decreased
example, they may be used to treat disorders associated with decreased
that affect the activity of (1) by expressing inactive proteins or to
supplement the patients own production of (1). Additionally, (1)
cuplement the patients own production of (1). Additionally, (1)
nucleic acids into a host cell and culturing the cell to express the
protein. (1) proteins and polymucleotides may be used to prevent,
diagnose and cract immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic antigen genomic
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK64950 and AAM82169

ACD76144 standard; DNA; 100 BP.

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ACD76144;

represent sequences used in the exemplification of the present invention

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RESULT 12
 The invention relates to a novel polymucleotide isolated and purified from a human gene having any one of 935 fully defined sequences as given in specification, or a sequence having a base substitution. The invention of further relates to: an oligonucleotide containing single nucleotide polymorphisms; a PCR primer set chosen from the combination of two DNA fragments from any one of 1220 fully defined sequences as given in specification; a labelling probe containing the SNP containing oligo; and a microarray equipped with the SNP containing the single nucleotide polymorphisms in human gene. The isolated human gene is also useful for diagnosis of disease and determination of side effect to a medical agent. The isolated human gene is also effect in detecting single nucleotide polymorphisms in a human gene. This polymorleolide sequence represents
 ö
 Novel polynucleotide useful for detecting single nucleotide polymorphisms
 human; single nucleotide polymorphism; microarray; side effect; gene; ds.
 73
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 65 recercadacreacacraderrerreacreacererererecadeserececereres
 TCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCCTCA
 Gaps
 Single nucleotide polymorphism detection human gene, SEQ ID No 607.
 .
0
 Length 121;
 24; Indels
Sequence 121 BP; 34 A; 19 C; 56 G; 12 T; 0 U; 0 Other;
 Sequence 121 BP; 24 A; 42 C; 40 G; 14 T; 0 U; 1 Other;
 DB 4;
 Score 22.6; DB 4;
Pred. No. 2.1e+03;
0; Mismatches 24
 Claim 1; SEQ ID NO 607; 704pp; Japanese.
 (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 ADF87024/c
ID ADF87024 standard; DNA; 121 BP.
 12-FEB-2002; 2002JP-00034717.
 12-FEB-2002; 2002JP-00034717.
 Query Match
Best Local Similarity 60.7%;
Matches 37; Conservative
 (first entry)
 WPI; 2003-820454/77.
 JP2003235571-A.
 in human gene.
 74 Ç 74
 5
C-5
 Homo sapiens.
 26-FEB-2004
 26-AUG-2003.
 invention
 14
 ADF87024;
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containing many identical probes. The probes are nucleotide sequences of 30-80 bases, are prepared ex situ from synthetic oligonucleotides and at least one includes a segment of at least 20 bases identical with, or complementary to, a segment of an open reading frame (orf) of Escherichia (orl) K12. The biochip is used for specific detection of gene expression in K12 and for determining the gene expression pattern, e.g. for diagnostic determination of which E. coli strains are present in the gut, and to determine the effects of e.g. growth media on gene expression. The biochip provides as comprehensive as possible detection of the K12.

C senome, with simultaneous analysis of many different genes with a single device, and comparison of gene expression between K12 and its mutants or other E. coli strains in a single experiment. Apart from qualitative and quantitative informattion about gene expression, it also allows measurements of population densities for the various strains. The use of synthetic oligonucleotides for preparation of probes allows free
 variation in probe length and ensures high purity (and thus selectivity, reactivity and reproducibility); also synthetic probes are generally shorter than probes prepared by polymerase chain reaction. ACD68731 to ACD81540 represent oligonucleotide probes used with the biochip described
 Biochip containing probes complementary with open reading frames in
Escherichia coli K12, useful for detecting gene expression and expression
 61
 9 ACGITICCITCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCC
 2 ACGITIGITACAAGGIAAAGGCGACGCCGCCATGAAGCAGCGCGTCGCTGCGAACGTCGC
 This invention describes a novel biochip comprising probe spots, each
 Gapa
 Biochip; gene expression; gut; diagnostic; detection; probe; ss.
 ö
 Length 100;
 42; Indels
 Sequence 100 BP; 24 A; 29 C; 28 G; 19 T; 0 U; 0 Other;
 Score 21.8; DB 8;
Pred. No. 3.5e+03;
0; Mismatches 42;
 E. coli K12 MG1655 biochip probe SEQ ID 7420
 Weber J;
 69 CCTCACAGTGCGCCGCCATGTGCCTGCAG 97
 Claim 3; Page 1159; 2004pp; German.
 Huber A,
 17-MAY-2001; 2001EP-00112179.
 17.7%;
52.8%;
 17-MAY-2001; 2001EP-00112179
(first entry)
 47; Conservative
 Drescher B,
 (MWGB-) MWG-BIOTECH AG
 Query Match
Best Local Similarity
 WPI; 2003-241155/24
 Escherichia coli
 in the invention
 EP1260592-A1.
 18-SEP-2003
 27-NOV-2002.
 Donner H,
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CATGTTAATGCGCCTGCATGCACA 90

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Gaps

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Indels

DB 10; Length 121;

Score 22.2; DB 10 Pred. No. 2.8e+03;

18.0%; 77.1%;

Mismatches

. 0

Conservative

Query Match Best Local Similarity Matches 27; Conserv

ACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTG 99 57 Acceccicacariecrecaccaecrecereres 23

65

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Gaps

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Indels

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ACH89320 standard; DNA; 111 BP.
 03-APR-2002; 2002US-00029386.
 03-APR-2002; 2002US-00029386
 (PENN/) PENN S G.
(RANK/) RANK D R.
(HANZ/) HANZEL D K.
 WPI; 2004-119264/12
 Rank DR,
 surveying tissues.
 Human; probe; ss;
 US2003194704-A1.
 (PENN/) PENN S
(RANK/) RANK D
 29-JUL-2004
 Homo sapiens
 16-0CT-2003
 ACH89320;
 Penn SG,
RESULT 13
 ACH89320
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AX10269-X12937 are human DNA fragments which contain biallelic polymorphic markers which have been isolated using the primers represented in AXC09121-X10268. The base occupying the polymorphic site is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments can be used in methods for determining polymorphic forms in an individual for use in e.g. forenaics, paternity testing or for phenotypic typing for diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyhan syndrome, muscular dystrophy, Miskott-Aldrich syndrome, Pabry's disease, familial hypercholesterolemia, polycystic kidney disease, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary appearance is inflammation, cancer, diseases of the nervous syndrome, osteogenesis imperfecta, acute intermittent porphyria, autoimmune diseases, inflammation, cancer, diseases of the nervous system, infection by pathogenic microorganisms, and characteristics such as longevity, appearance (e.g. baldness, obesity), strength, speed, and ongrevity, and susceptibility or receptivity to particular drugs or therapeutic treatments. The isolated polymorphic nucleic acid segments can also be used to produce medicaments for the treatment or prophylaxis of such diseases.
 Polymorphism; biallelic; human; forensic; paternity testing; disease; detection; phenotypic typing; characteristic; infection; hereditary; autoimmune disease; cancer; inflammation; drug; therapy; medicament;
 New isolated nucleic acid segments from the human genome - used for determining polymorphic forms for use in e.g. forensics, paternity testing or phenotypic typing for disease.
 DB 12; Length 111;
 65 ACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTG 105
Sequence 111 BP; 18 A; 35 C; 30 G; 28 T; 0 U; 0 Other;
 19 AGCCCTCACAGAGCTTGCTCCTGTGTCAGCAGAGTGGCTG 59
 Human biallelic polymorphic DNA fragment stSG3935.
 3.6e+03
 0; Mismatches
 Score 21.8;
 Pred. No.
 (WHED) WHITEHEAD INST BIOMEDICAL RES.
 Claim 1; Page 286; 310pp; English.
 AAX12744 Standard; DNA; 120 BP.
 Hudson T;
 17.7%;
 96US-0030455P.
 97WO-US020313
 (first entry)
 Local Similarity 70.7
Les 29; Conservative
 treatment; marker; ss.
 Wang D,
 WPI; 1998-286974/25.
 Homo sapiens.
 WO9820165-A2
 0S-NOV-1997;
 06-NOV-1996;
 30-MAR-1999
 14-MAY-1998.
 ES,
 AAX12744;
 Query Match
 Lander
 Best Loc
Matches
 RESULT 14
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 The invention relates to a nucleic acid probe for measuring human gene expression, comprising any of the 27,400 fully defined nucleotide expression, comprising any of the 27,400 fully defined nucleotide expression, comprising any of the 6888 annion acid acquences conding at least 8 annio acids of any of the 6888 annion acid acquences fully defined in the specification. The probe is a single exon probe that thybridises under high stringency conditions to a nucleic acid molecule dypridises under high stringency conditions to a nucleic acid molecule addressable set of single exon nucleic acid probes for measuring human cells or tissues. Also included are a spatially-addressable set of single exon nucleic acid molecule comprising a purality of single exon microarray for measuring human gene expression, a method of and addressably isolatable or amplifiable from the plurality), a single commenced above, where each of the plurality of probes in separately and addressably isolatable or amplifiable from the plurality), a single contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of any of the above-mentioned amino acid contiguous amino acids of active acid active active active acid active acid active acid active
 New human genome-derived single exon nucleic acid probes useful for human gene expression analysis, for identifying or characterizing alternative splicing events, for assessing genomic alterations or as tools for
 Human; probe; 88; gene expression; single exon probe; microarray; alternative splicing event; genomic alteration.
 Human genome derived single exon probe #22515.
 Claim 1; SEQ ID NO 22515; 80pp; English.
 Hanzel DK;
 (first entry)
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Score 21.6; DB 2; Length 120; Pred. No. 4.2e+03;

17.6%;

Query Match Best Local Similarity

Sequence 120 BP; 25 A; 37 C; 30 G; 27 T; 0 U; 1 Other;

prophylaxis of such diseases

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 The present sequence is one of a large number of 5' ESTS derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTS are not well suited for isolating onNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTS are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
 Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
 New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
 Gaps
 Gaps
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 Length 119;
 Claim 1; SEQ ID NO 15214; 71pp + Sequence Listing; English.
 GTTTCCCACAGGCTGAGTACTATGGGGTCACAACCTTCCTGGAC 118
 21; Indels
 Mismatches 14; Indels
 11 GTTTCCTTCAGACTGAGACAGCTGGGTCCCAGCCTCACCTGAC 54
 Sequence 119 BP; 19 A; 44 C; 32 G; 24 T; 0 U; 0 Other;
 Score 21.4; DB 3;
Pred. No. 4.9e+03;
0; Mismatches 21;
 Human secreted protein 5' EST, SEQ ID NO: 15214.
 Duclert A, Giordano J;
 expression and secretion vectors
 AAC11139 standard; cDNA; 119 BP.
 .
0
 17.4%;
61.8%;
 21-FEB-2000; 2000EP-00200610
 99US-0122487P
 06-OCT-2000 (first entry)
30; Conservative
 34; Conservative
 Dumas Milne Edwards J,
 Query Match
Best Local Similarity
Matches 34; Conservat
 WPI; 2000-500381/45.
 (GEST) GENSET.
 26-FEB-1999;
 EP1033401-A2.
 Homo sapiens
 06-SEP-2000.
 75
 AAC11139;
Matches
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Search completed: January 31, 2005, 21:12:28 Job time : 272 secs

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Title: Perfect score:

Sequence:

OM nucleic

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Run

Scoring table:

Searched:

Minimum DB Maximum DB

Database

```
Sequence 210, App
Sequence 31791, A
Sequence 31869, A
Sequence 1348, Ap
Sequence 1348, Ap
Sequence 24132, A
Sequence 25943, A
Sequence 25943, A
Sequence 27983, A
Sequence 2152, A
Sequence 2152, A
Sequence 2152, A
Sequence 21933, A
Sequence 21033, A
Sequence 27083, A
Sequence 27083, A
Sequence 27083, A
Sequence 27083, A
Sequence 32748, A
Sequence 32748, A
 97 cccadecedeciriocerrecrerirerecedecedecedecedecederecedeceded 38
 Sequence 209, A Sequence 210, A Sequence 209, A Sequence 209, A Sequence 210, A Sequence 210, A Sequence 209, A
 Sequence 383, A
Sequence 298, A
Sequence 299, A
 CCCAGCCTCACCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCGTGTGCCCTGCAGT
 Sequence 4678, Application US/09867701
| Sequence 4678, Application US/09867701
| SEDERAL INFORMATION:
| APPLICANT: Adjate, Paul A. |
| APPLICANT: Adjate, Paul A. |
| APPLICANT: Harlocker, Susan L. |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER |
| FILE REFERENCE: 210121.497 |
| CURRENT FALICATION NUMBER: US/09/867,701 |
| CURRENT FILING DATE: 2001-05-29 |
| NUMBER OF SEQ ID NOS: 10912 |
| SEQ ID NO 4678 |
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 37; Indels
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0 US-09-918-787-210

6 US-10-209-787-210

6 US-10-209-787-210

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US-10-045-674-298
US-10-045-674-299
 0; Mismatches
 Score 25.8; Pred. No. 76;
 99 GTGGGTGCTGCTCAGCCGGGACCCC 123
 37 Accrecécréecreéecécéakécee 13
 21.0%;
56.5%;
 118
118
9
9
9
 Conservative
 TYPE: DNA
CORGANISM: Homo sapien
US-09-867-701-4678
 l Similarity
48; Conserva
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 Query Match
Best Local
 Matches
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 Sequence 4678, Ap
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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 Description
 Published Applications NA:*

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 GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
 US-09-867-701-4678

US-10-674-124A-21157

US-09-818-875-337

US-09-818-875-338

US-10-209-787-338

US-10-209-787-338

US-10-21-185-338

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
 Length
 97
 seq length: 0
seq length: 123
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Match 1
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RESULT

Sequence

22.2

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Score

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APPLICANT: Kaniec, Eric B.
APPLICANT: Gamper, Howard B.
APPLICANT: Gamper, Howard B.
APPLICANT: Raniec, Michael C.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
TITLE OF INVENTION: Stranded Oligonucleotides
TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: Napro-4
CURRENT APPLICATION NUMBER: US/09/818,875
CURRENT FILING DATE: 2001-03-27
FRIOR APPLICATION NUMBER: US 60/192,176
FRIOR PILING DATE: 2000-03-27
FRIOR FILING DATE: 2000-03-27
FRIOR FILING DATE: 2000-06-01
FRIOR FILING DATE: 2000-06-01
FRIOR FILING DATE: 2000-06-01
FRIOR FILING DATE: 2000-06-01
 Sequence 337, Application US/10209787
Publication No. US20030217377A1
GENERAL INFORMATION:
APPLICANT: Kmiec, Fic B.
APPLICANT: Rice, Michael C.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
 118 cécriragiecrecciesesesesécresresresdescrecerricares 59
 10 CGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCC 69
 10 COTTICCTICAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCC
 4 decrinaciecrecidesesesedecresresesesesecresecrineresesasarretre
 Gaps
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 DB 10; Length 121;
 Query Match 18.7%; Score 23; DB 10; Length 121; Best Local Similarity 54.0%; Pred. No. 6.4e+02; Matches 47; Conservative 0; Mismatches 40; Indels
 40; Indels
 Pred. No. 6.4e+02;
0; Mismatches 4(
 0; Mismatches
 70 CTCACAGTGCGCCGCCATGTGCCTGCA 96
 58 recrerciccececercreceada 32
 70 CTCACAGTGCGCCGCCATGTGCCTGCA 96
 Sequence 338, Application US/09818875; Publication No. US20030051270A1; GENERAL INFORMATION:
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 4385
SOFTWARE: Friedman macro Napro4
 NUMBER OF SEQ ID NOS: 4385
SOFTWARE: Friedman macro Napro4
SEQ ID NO 338
 ch 18.7%;
1 Similarity 54.0%;
47; Conservative
 TYPE: DNA ORGANISM: Homo sapiens
 Best Local Similarity
 RESULT 5
US-10-209-787-337/c
 US-09-818-875-337
 US-09-818-875-338
 SEQ ID NO 337
 Query Match
 TYPE: DNA
 Matches
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 arm and
 Genomic Alterations with Modified Single
 OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of OTHER INFORMATION: sequence listing upward to telomere on chrosomal short OTHER INFORMATION: 5'-terminus of this base sequence: 76372
 12 TITCCITCAGACTGAGGACAGCTGGGTCCCAGCTGACACAGAGGCTAGACCCCCT 71
 OTHER INFORMATION: Located on chromosome 14
PERTURE:
OTHER INFORMATION: Distance between a terminus base of telomere on
OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
OTHER INFORMATION: sequence : 104184465
 Gaps
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 APPLICANT: INGN, HIGHORDING
TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
TITLE OF INVENTION: GENE MAPPING MARKERS
FILE REFERENCE: ORIN-033-09-26
FRIOR APPLICATION NUMBER: 10/257,511
FRIOR APPLICATION NUMBER: 10/257,511
FRIOR PILING DATE: 2000-10-30
FRIOR PILING DATE: 2000-10-30
FRIOR PILING DATE: 2000-04-13
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FRIOR PILING DATE: 2002-02-28
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FRIOR FILING DATE: 2002-12-09
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FRIOR FILING DATE: 2002-12-09
 Length 101;
 Indels
 Score 23.2; DB 18;
Pred. No. 5.5e+02;
0; Mismatches 33;
 APPLICANT: Gamper, Howard B.
APPLICANT: Gamper, Howard B.
APPLICANT: Rice, Michael C.
TITLE OF INVENTION: Targeted Chromosomal Genomic
TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: Nappro-4
CURRENT APPLICATION NUMBER: US/09/818,875
CURRENT FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR APPLICATION NUMBER: US 60/192,179
PRIOR FILING DATE: 2000-03-27
 Sequence 21157, Application US/10674124A Publication No. US20040197797A1 GENERAL INFORMATION:
 Sequence 337, Application US/09818875
Publication No. US20030051270A1
GENERAL INFORMATION:
 FEATURE:
OTHER INFORMATION: DID22N_0010585
FEATURE:
 18.9%;
56.6%;
 72 CACAGTGCGCCGCAT 87
 41 cacrerererecen 26
 APPLICANT: INOKO, Hidetoshi
 Ouery Match
Best Local Similarity 56.61
Matches 43; Conservative
 TYPE: DNA
ORGANISM: Homo sapiens
 US-09-818-875-337/c
 SEQ ID NO 21157
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GENERAL INFORMATION:

APPLICANT: Kmlec, Eric B.
APPLICANT: Kmlec, Eric B.
APPLICANT: Gamper, Howard B.
APPLICANT: Gamper, Howard B.
APPLICANT: Gamper, Howard C.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: NaPro-4CON
CURRENT APPLICATION NUMBER: US/10/261,185
CURRENT FILING DATE: 2001-09-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-06-01
SOFWWARE: VS 60/208,538
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 4385
SOFWWARE: Friedman macro Napro4
SEQ ID NO 337

**MANDER OF SEQ ID NO 337
 US-10-201-185-138-34

Sequence 338, Application US/10261185

Publication No. US20040014057A1

GENERAL INFORMATION:
APPLICANT: Kamiec, Eric B.
APPLICANT: Kamiec, Eric B.
TILE OF INVENTION: Targed Chromosomal Genomic Alterations with Modified Single TILE OF INVENTION: Stranded Oligonucleotides
TILE OF INVENTION: Stranded Oligonucleotides
TILE OF INVENTION: Stranded Oligonucleotides
TILE OF INVENTION: STRANDER: US/10/261,185
CURRENT FILING DATE: 2002-09-27

PRIOR PEPLICATION NUMBER: PCT/US01/09761

PRIOR FILING DATE: 2000-03-27

PRIOR PELING DATE: 2000-03-27

PRIOR PELING DATE: 2000-03-27

PRIOR PILING DATE: 2000-06-01

PRIOR PILING DATE: 2000-06-01

PRIOR PILING DATE: 2000-06-01

PRIOR PILING DATE: 2000-06-01
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 Length 121;
 40; Indels
 Score 23; DB 16;
Pred. No. 6.4e+02;
0; Mismatches 40
 96
 64 recreteriscicioserererecensos 90
 58 rccrcrerecececercrereceage 32
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 Sequence 317, Application US/10261185; Publication No. US20040014057A1
GENERAL INFORMATION:
 Query Match
Best Local Similarity 54.0%;
Matches 47; Conservative
 Homo sapiens
 US-10-261-185-337/c
 us-10-261-185-337
 ORGANISM:
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 GENERAL INFORMATION:

APPLICANT: Gamper, Howard B.
APPLICANT: Raice, Michael C.
TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single
TITLE OF INVENTION: Stranded Oligonucleotides
TITLE OF INVENTION: Stranded Oligonucleotides
FILE REFERENCE: Napro-4
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US 60/192,176
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PRIOR APPLICATION NUMBER: US 60/192,176
PRIOR PILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-03-27
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/208,538
PRIOR FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: US 60/204,989
PRIOR FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 4386
NUMBER OF SEQ ID NOS: 4386
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 118 cécriradrecrecerégéecaécrecreagecrececrirecressagarrerer 59
 4 cécriragiedreciregégéadadiciregregadadicirecidadirectron 63
 10 CGTTTCCTTCAGACTGAGGACAGCTGCCAGCCTCACCTGACACAGGGCTAGACCCC
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0
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 DB 15; Length 121; 6.4e+02;
 Length 121;
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 Score 23; DB 15;
Pred. No. 6.4e+02;
0; Mismatches 40
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 Score 23; DB 1
Pred. No. 6.4e4
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 PRIOR PELLING DATE: 2002-07-30

PRIOR FILING DATE: 2001-03-7

PRIOR PILING DATE: 2001-03-27

PRIOR APPLICATION NUMBER: US 60/192,176

PRIOR PILING DATE: 2000-03-27

PRIOR PILING DATE: 2000-03-27

PRIOR FILING DATE: 2000-06-01

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PRIOR PILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: US 60/244,989

PRIOR PILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 4385

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LENGTH: 121
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CURRENT FILING DATE: 2002-07-30
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Publication No. US20030217377A1
GENERAL INFORMATION:
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54.0%;
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Best Local Similarity 54.0%;
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 ORGANISM: Homo sapiens US-10-209-787-338
 ORGANISM: Homo sapiens
US-10-209-787-337
 Query Match
Best Local Similarity
Matches 47; Conserva
 SEQ ID NO 338
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Query Match
Best Local Similarity
Matches 47; Conserv
 RESULT 11
US-10-242-535A-10710/c
 TYPE: DNA
ORGANISM: Human
 US-10-681-074-338
 LOCATION:
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 APPLICANT: KAIEC, ERIC B.
APPLICANT: KAIEC, ERIC B.
APPLICANT: WAN BRABANT, ANJA
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REDUCING SCREENING IN
TITLE OF INVENTION: OLIGOWUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
FILE REFERENCE: NaPro-18 US
CURRENT APPLICATION NUMBER: US/10/681,074
CURRENT PILING DATE: 2003-10-07
PRIOR APPLICATION NUMBER: US 60/453,360
PRIOR APPLICATION NUMBER: US 60/416,983
PRIOR RILING DATE: 2003-03-07
PRIOR RILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 4375
SOFTWARE: Patentin version 3.2
SEQ ID NO 337
 Sequence 338, Application US/10681074
Publication No US20040175722A1
FURDIAGATION:
APPLICANT: UNROMATION:
APPLICANT: VAN BRABANT, ANJA
APPLICANT: VAN BRABANT, ANJA
TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
TITLE OF INVENTION: OLIGONUCLEOTIDE-DIRECTED NUCLEIC ACID SEQUENCE ALTERATION
FILE REPERENCE: NaPro-18 US
CURRENT APPLICATION NUMBER: US/10/681,074
CURRENT PILING DATE: 2003-10-07
PRIOR FILING DATE: 2003-03-07
PRIOR FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: US 60/453,360
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 10 CGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCC 69
 118 cdcriragiacroccidadadadadercaraadacriccccirricriacadanerecia so
 10 CGTTTCCTTCAGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCC 69
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 Length 121;
 40; Indels
 40; Indels
 Score 23; DB 17;
Pred. No. 6.4e+02;
0; Mismatches 40
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54.0%; Pred. No. e...
0; Mismatches
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 Sequence 337, Application US/10681074 Publication No. US20040175722A1 GENERAL INFORMATION:
 SOFTWARE: Friedman macro Napro4
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 TYPE: DNA
ORGANISM: Homo sapiens
 TYPE: DNA
ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
Matches 47; Conserv
 .10-681-074-337/c
) UKGANATAN: DUNING
US-10-261-185-338
 US-10-681-074-338
 US-10-681-074-337
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APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR PLILNG DATE: 2002-09-28
PRIOR PLILNG DATE: 2001-07-13
PRIOR PLILNG DATE: 2001-07-13
PRIOR PLILNG DATE: 2001-03-12
PRIOR PLILNG DATE: 2001-03-12
PRIOR PLILNG DATE: 2001-03-12
PRIOR PLILNG DATE: 2001-03-12
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PRIOR FILING DATE: 2001-03-13
PRIOR FILING DATE: 2001-03-14
PRIOR FILING DATE: 2001-03-15
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 ch 18.7%; Score 23; DB 17; Length 121; I Similarity 54.0%; Pred. No. 6.4e+02; 47; Conservative 0; Mismatches 40; Indels
 70 CTCACAGTGCGCCGCCATGTGCCTGCA 96
 64 recrerchicececearcreceaea 90
 ; Sequence 10710, Application US/10242535A; Publication No. US20040013663A1; GENERAL INFORMATION:
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PRIOR FILING DATE: 2002-10-07
NUMBER OF SEQ ID NOS: 4375
SOFTWARE: PatentIn version 3.2
SEQ ID NO 338
LENGTH: 121
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; OTHER INFORMATION: n is a,
US-10-242-535A-10710
 LOCATION: (17) ... (17)
OTHER INFORMATION: n is a,
 ON: (29)..(29)
INFORMATION: n is a,
 APPLICANT: Chondrogene Inc. APPLICANT: Liew, C.C.
 LOCATION: (3)...(3)
OTHER INFORMATION: n is
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OTHER INFORMATION: n is
 TYPE: DNA
ORGANISM: Homo sapiens
 NAME/KEY: misc_feature
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LOCATION: (17)..(17)
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NAME/KEY: misc_feature
 NAME/KEY: misc feature
 NAME/KEY: misc_feature
 NAME/KEY: misc_feature
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 Sequence 10710, Application US/10085783A

Publication No. US20040037841A1

GENERAL INFORMATION:

APPLICANT: Liew, C.C.

TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis

FILE REFERENCE: 4231/2002

CURRENT FILING DATE: 2002-02-28

FRIOR PRILOR APPLICATION NUMBER: US/10/085,783A

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-07-13

PRIOR FILING DATE: 2001-03-05

PRIOR FILING DATE: 2001-02-28

FRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

PRIOR FILING DATE: 2001-02-28

SOFTWARE: Patentin version 3.2

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SEQ. ID NOS: 58994
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 86 CGTGCCCGTCTGCCCGAGGGCAGGATCCCCTCNTCCTGTGNTGGCTCGTGCCNAANTC 27
 86 ccereccercreceaececaecaecaececerenecererenececereres
 Gaps
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 Length 117;
 Length 117;
 Indels
 Indels
 Score 22.2; DB 16;
Pred. No. 1.2e+03;
0; Mismatches 33;
 33;
 Score 22.2; DB 10
Pred. No. 1.2e+03,
0; Mismatches 33
 | LOCATION: (52) ... (52) | OTHER INFORMATION: n is a, c, g, or t US-10-085-783A-10710
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54.2%;
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 LOCATION: (17)...(17)
OTHER INFORMATION: n is a,
 LOCATION: (29)...(29)
OTHER INFORMATION: n is a,
 Query Match
Best Local Similarity 54.2³
Matches 39; Conservative
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 LOCATION: (44)..(44)
OTHER INFORMATION: n is a,
 99 GIGGIGCIGCI 110
 TTTGGATCCNCT 15
 26 TTTGGATCCNCT 15
 LOCATION: (3). (3)
OTHER INFORMATION: n is
 OTHER INFORMATION: n is
 NAME/KEY: misc feature
 NAME/KEY: misc_feature
 NAME/KEY: misc feature
 NAME/KEY: misc feature
 NAME/KEY: misc_feature
 NAME/KEY: misc_feature
Query Match
Best Local Similarity
----- 39; Conserve
 -10-085-783A-10710/c
 ORGANISM: Human
 LOCATION:
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AECMICA.X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
 ö
 Gaps
 Gaps
 ö
 ö
 Length 111;
 CTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.9

CTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.7

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4

OTHER INFORMATION: STESSEOT HIT: P35624, EVALUE 1.20e+00

CTHER INFORMATION: NT HIT: AF025309.2, EVALUE 9.10e-02

CTHER INFORMATION: EST_HUMAN HIT: BG957228.1, EVALUE 1.30e-01

US-10-029-386-22515
 Length 121;
 Indele
 Indels
 65 ACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTG 105
 Score 21.8; DB 15;
Pred. No. 1.6e+03;
0; Mismatches 12;
 17.2%; Score 21.2; DB 10; 55.4%; Pred. No. 2.5e+03; tive 0; Mismatches 33;
Sequence 22515, Application US/10029386; Publication No. US20030194704A1; GENERAL INFORMATION:
 ; Sequence 209, Application US/09818875; Publication No. US20030051270A1
; GENERAL INFORMATION: GENERAL INFORMATION:
 ch
1 Similarity 70.7%;
29; Conservative
 41; Conservative
 TYPE: DNA ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
Matches 41; Conserval
 Query Match
Best Local Similarity
 RESULT 14
US-09-818-875-209/c
 SEQ ID NO 22515
 FEATURE:
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Sequence 210, Application US/09818875

| Publication No. US20030051270A1
| Publication No. US20030051270A1
| GENERAL INFORMATION:
| APPLICANT: Kaniec, Exic B.
| APPLICANT: Kaniec, Faic B.
| APPLICANT: Ramper, Howard B.
| APPLICANT: Rice, Michael C.
| TITLE OF INVENTION: Targeted Chromosomal Genomic Alterations with Modified Single FILE OF INVENTION: Stranded Oligonucleotides
| TITLE OF INVENTION: NUMBER: US 60/192,176
| PRIOR FILING DATE: 2000-03-27
| PRIOR PELICATION NUMBER: US 60/244,989
| PRIOR PILING DATE: 2000-06-01
| PRIOR PILING DATE: 2000-10-30
| NUMBER OF SEQ ID NOS: 4385-050 NUMBER: Friedman macro Napro4
| SEQ ID NO 210
| TATLE OF TITLE ö
23 CTGAGGACAGCTGGGTCCCAGCCTCACCTGACAGGCTAGACCCCCTCACAGTGCGCC 82
 121 crideciaciácicoros adacrico crirroracea a protrocrororación 62
 1 chadadachtchagaadachtcchrrchracadaantchtrchrchdadcac
 23 CTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCCCTCACAGTGCGCC
 Gaps
 .
0
 Query Match 17.2%; Score 21.2; DB 10; Length 121; Best Local Similarity 55.4%; Pred. No. 2.58+03; Matches 41; Conservative 0; Mismatches 33; Indels 0
 Search completed: January 31, 2005, 23:05:45
Job time : 308 secs
 61 GGTCTCTCCCAGGA 48
 83 GCCATGTGCCTGCA 96
 83 GCCATGTGCCTGCA 96
 61 Gercrereceagga 74
 TYPE: DNA
CORGANISM: Homo sapiens
US-09-818-875-210
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| | C9912 | | C9012 | C901
 ptodata/1/pna/US6022_COMB.seq:*
ptodata/1/pna/US6023A_COMB.seq:*
ptodata/1/pna/US6023B_COMB.seq:*
 January 31, 2005, 19:01:47; Search time 2458 Seconds (without alignments) 4503.816 Million cell updates/sec
 273
 1 atggagcactaccggaaagc......ccaagctacgtttccttcag
 55031126
 CGM2 6/ptodata/1/pna/PCTUS1 COMB.seq:*

(GGM2 6/ptodata/1/pna/DSC COMB.seq:*

(GGM2 6/ptodata/1/pna/USOB COMB.seq:*

(GGM2 6/ptodata/1/
 5.1.6
Compugen Ltd.
 44308572 segs, 20275418765 residues
 Total number of hits satisfying chosen parameters:
 GenCore version
Copyright (c) 1993 - 2005
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 nucleic search, using sw model
 US-10-057-813-13_COPY_1_273
273
 Pending Patents NA Main: * /cgn2_6/ptodata/1/pna/
 Gapop 10.0 , Gapext 1.0
 seq length: 0
seq length: 273
 Title:
Perfect score:
 Scoring table:
 1
 88
 OM nucleic
 ••
 Sequence:
 Searched:
 Minimum I
Maximum I
 Database
 Run on:
```

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117: /cgn2_6/ptodata/1/pna/US6051_COMB.seq:*
118: /cgn2_6/ptodata/1/pna/US6052_COMB.seq:*
119: /cgn2_6/ptodata/1/pna/US6053_COMB.seq:*
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121: /cgn2_6/ptodata/1/pna/US6055_COMB.seq:*
122: /cgn2_6/ptodata/1/pna/US6055_COMB.seq:*
123: /cgn2_6/ptodata/1/pna/US6055_COMB.seq:*
123: /cgn2_6/ptodata/1/pna/US6057_COMB.seq:*
124: /cgn2_6/ptodata/1/pna/US6058_COMB.seq:*
125: /cgn2_6/ptodata/1/pna/US6059_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Description    | equence 2456,   | equence 8863,     | quence 2841     | Sequence 352      | quence 2389                           | equence 126        | ednence 768     | Seguence 6668, Ap | equence 141     | equence 451     | equence 141     | equence 506     | equence 304     | equence 304    | equence 1037,   | equence 161     | equence 1610    | equence 1610      | equence 1305     | equence 3009    | equence 130     | equence 1878    | equence 73,    | equence 3013      | equence 3013     | equence 73,    | ednence          | equence 3710    | equence 1267     | equence 1609    | e 7664             | edneuce Tena                             | equence 28833, | seduence 11355                    | quence 22, Appl | equence 10618,    | equence 10618,   | equence 15324,   | equence 15324, | equence 15324,   | equence 2187, A | equence 790 | equence 2052. A | quence 16308,   |
|----------------|-----------------|-------------------|-----------------|-------------------|---------------------------------------|--------------------|-----------------|-------------------|-----------------|-----------------|-----------------|-----------------|-----------------|----------------|-----------------|-----------------|-----------------|-------------------|------------------|-----------------|-----------------|-----------------|----------------|-------------------|------------------|----------------|------------------|-----------------|------------------|-----------------|--------------------|------------------------------------------|----------------|-----------------------------------|-----------------|-------------------|------------------|------------------|----------------|------------------|-----------------|-------------|-----------------|-----------------|
| αı             | US-08-856-624-2 | S-09-540-766-8863 | S-08-941-869A-2 | 5-09-540-208-3526 | 08-438-5/1A-2389<br>-08-540-2335-1261 | 3-03-340-23D-12618 | -06-536-334-688 | 08-812-505-1      | -08-978-620-141 | -09-540-229-451 | -60-013-529-141 | -08-951-197-506 | -09-539-806-304 | 9-539-806B-304 | -60-027-249-103 | 09-539-800-1610 | -09-539-800B-16 | -09-539-800C-1610 | -09-014-441-1305 | -09-540-212A-30 | 60-034-841-1305 | -09-540-213-187 | -08-901-902-73 | -09-539-806-30137 | -09-539-806B-301 | -60-023-379-73 | -08-8/9-863-3710 | -08-8/9-863A-3/ | -09-540-213-1267 | VAL 4666 043 00 | 8-09-340-2330-7664 | S-00-1033-1033-1033-1033-1033-1033-1033- | 8-09-3334-268  | -0-03-040-11000<br>-00-410 160 00 | 08-413-130-22   | -09-540-499-10618 | -09-540-499B-106 | -09-539-800-1532 | -09-539-8      | -09-539-800C-153 | -08-923-902-218 |             | -08-801-504-205 | -09-540-499-163 |
| DB             | 13              |                   | 7.              | 7 C               | y C                                   |                    |                 | 13                | 14              | 24              | 99              | 14              | 23              | 23             | 67              | 23              | 23              | 23                | 15               |                 | 89              |                 | 4 6            | 23                | 2 (              | 9 5            | 7 -              | 2 5             |                  | 9 6             | , L                |                                          | 9 6            |                                   | , ,             | 7 7               | 47               | 53               | 23             | 23               | 14              | 24          | 13              | 24              |
| Length         | 4               | oι                | ~ 1             | ` <               | * 4                                   | r vo               | ) LC            | 262               | w               | w               | S               | 10              | in              | 10             | ın              |                 | 10              | · ^ ·             |                  |                 |                 |                 |                |                   |                  |                | 2 6              |                 |                  |                 |                    |                                          |                |                                   |                 |                   |                  |                  |                | 224              |                 | 234         |                 | Τ.              |
| Query<br>Match |                 | vi o              |                 | , r               | ٠,                                    | ·                  |                 |                   | ä               | ä               | ÷               | ö               | ö               | . ·            | <u>.</u>        | ٠.<br>د         | <u>.</u>        |                   | <u>.</u>         | ή,              | ÷.              | ٠.              | ٠.             | ٠,                | : -              | ٠,             | ٠.               |                 | ٠.               | ٠.              | 67.5               | ٠.                                       | ٠:             | :                                 | :               | :                 | : .              | <u>.</u>         | <u>.</u>       | ᆣ.               | _•              | <u>.</u>    | •               |                 |
| Score          | 226             | ٧r                |                 | 4 -               |                                       | 10                 | 0               | ത                 | σ               | σ               | o               | σ.              | ത               | σ, α           | σ,              | n o             | <b>a</b>        | <b>T</b>          | Th. 6            | T (             | 7 6             | ٠.0             | 0              | 0 0               | o a              | 0 0            | 184              | ο α             | קר               | ? &             | 183.4              | 18                                       | m              |                                   | ) LC            | 2 11              | n t              | nı               | 0 1            | 997              | 997             | 166         | 157             | 157             |
| Result<br>No.  | н (             | 7 6               | 7               | י ני              | n vo                                  | , _                | 80              | 6                 | 10              | 11              | 12              | 13              | 14              | 12             | 91              | 7.7             | 18              | 19                | 0 .              | 7 7             | 7 6             | 2 2             | # U            | 0 4               | 0 0              | 40             | 0 0              | ) C             | 3.0              | 3.5             | 33                 | 34                                       | 35             | 36                                | 37              | ה α<br>ה          | ם<br>ס           | n •              | 0 7            | 4.4              | 4.              | 43          | 4.              | 45              |

## ALIGNMENTS

```
RESULT 1
US-08-856-624-2456
; Sequence 2456, Application US/08856624
; GENERAL INFORMATION:
```

RESULT 2

|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | o<br>,                                                                                                       | 107                 | 167                                                            | 227                                                              |                                                |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------|---------------------|----------------------------------------------------------------|------------------------------------------------------------------|------------------------------------------------|
| APPLICANT: Gooding, Douglas H. APPLICANT: Stuve, Laura L. APPLICANT: ACCOUNT: Stuve, Laura L. APPLICANT: ACCOUNT: ACCOUNT: ACCOUNT: APPLICANT: Naughton, Ingrid E. APPLICANT: Naughton, Ingrid E. APPLICANT: Naughton, Rebecca E. APPLICANT: Naughton, Ridmon Deloyepertides and October E. APPLICANT: Naughton, SIGMOID DENOCARCINOMA. CORRESPONDER ADDRESS: ACCOUNTER; DATA PROBLESS: ACCOUNTER TRANSMICAL PROBLESS: ACCOUNTER TRANSMICAL COUNTER PARAMACEUTICALS, INC. STREET: 3174 PORTER DRIVE COUNTER; USA COUNTER DRIVE COUNTER; USA COUNTER DRIVE COUNTER; USA COUNTER DRIVE COUNTER REPAIR STEFFER PORTER APPLICATION NAUGHS: USA COUNTER TRANSMICATION DATA: APPLICATION NAUGHS: USA COUNTER SEPTIONER: GO/017, 190 FILING DATE: HERMITH: CLASSIFICATION NAUGHS: GO/017, 190 FILING DATE: REPTEMBER: GO/017, 190 FILING DATE: REPTEMBER: GO/017, 100 ATTORNEY APPLICATION NAUGHS: GO/017, 100 ATTORNEY AGNIT INFORMATION: NAME: CERRONE, MICHAER SGO, 100 ATTORNEY AGNIT INFORMATION: NAME: CERRONE, MICHAER SGO, 100 ATTORNEY AGNIT INFORMATION: TELEPHONE: (415) 865-6555 TELEPHONE: (415) 865-655 TELEPHONE: (415) 865-655 TELEPHONE: GO/017, 100 SEQUENCE CHARACTERIFICS: LENGTH: 264 base pairs TELEPHONE: (415) 865-655 TELEPHONE: COUNTER TREE COUNTER T                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 82.8%; Score 226; DB 13; Length 264;<br>100.0%; Pred. No. 6.4e-51;<br>vative 0; Mismatches 0; Indels 0; Gaps | GTCCGAGATGGCAGC<br> | TCGCAACCTGCTGGGGTTTGGCTTCGGGTTGGAGGCGCGGCAGTGCTCGGCATGTAGT 167 | GITCICAGGITCIGGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGAITGTCAAGCG 227 | GCGGGTCCCAGGCCTGCACCAGCTACCATTTCCTTCAG 273<br> |
| T1: GG<br>T1: St<br>St<br>T1: St<br>T1: De<br>T1: De<br>T1: De<br>T1: De<br>T1: De<br>T1: De<br>T2: De<br>T2: De<br>T2: De<br>T2: De<br>T2: De<br>T3: De<br>T3: De<br>T3: De<br>T3: De<br>T4: De<br>T4: De<br>T4: De<br>T5: De<br>T6: De | mil.                                                                                                         | <u>8</u> —8         | 00<br>                                                         |                                                                  | 8<br>                                          |
| APPLICANT: Stude, LAPPLICANT: Stude, LAPPLICANT: Stude, LAPPLICANT: Stude, LAPPLICANT: Stude, LAPPLICANT: Stude, Laughton APPLICANT: Delegean APPLICANT: Naingler TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES: CORRESPONDENCE ADDRE STREET: 3174 PORT CITY: PALO ALTO STREET: 3174 PORT CITY: PALO ALTO STREET: 3174 PORT CITY: PALO ALTO STREET: ADDREADEL FOOMPOUTER: COMPUTER: FOOMPOUTER: DADRE SOFTWARE: NOOF PECUNTY: DADRE SOFTWARE: NOOF PECUNTY: DADRE SOFTWARE: NOOF PECUNTY APPLICATION DATE: HERE FILING DATE: MAY: PRIOR APPLICATION NUMBER FILING DATE: MAY: TELEPONTY FOR SEQ ID SEQUENCE CHRACTERIS INFORMATION FOR SEQ ID SEQUENCE CHARACTERIS SING TONE INFORMATION FOR SEQ ID SEQUENCE CHARACTERIS COUNCE: Innear MOLECULE TYPE: cDNA INMEDIANE SOURCE: CLONE: 1929519                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | Query Match<br>Best Local Similarity<br>Matches 226; Conser                                                  | 48<br>0 1<br>0 0    | 108 T<br>61 T                                                  | 168 G<br>121 G                                                   | 228 G<br>181 G                                 |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | ōğ≌                                                                                                          | 중 음                 | දු පු                                                          | · & · &                                                          | 8 %                                            |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |                                                                                                              |                     |                                                                |                                                                  |                                                |

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54 ArgeAgcacraccegaAAGcrescreterAGAGcreccAGCGCCrreccAArGCCCCAG 113
 114 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG 173
 GGGTTGGCTCTGGGTTGGAGGCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 180
 174 GGGTTGGCTCTGGGTTGGAGGCGCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 233
 APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Laura I.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mushton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF MALE REPRODUCTIVE TISSUE
FILE REFERENCE: PD-1029 CIP
CURRENT APPLICATION NUMBER: US/09/540,208
CURRENT APPLICATION DATE: 2000-03-31
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 70811
SOFTWARE: PERL PROGRAM
SEQ ID NO 35269
LENGTH: 271
 ö
 Length 271;
 ; Score 218; DB 14; Leng...
---d, No. 9.7e-49; Indels
 181 GGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGAT 218
 GGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGAT 271
 PRILING DATE: HERBAITH
CLASSIFICATION NUMBER: US/08/941,869A
FILING DATE: HERBAITH
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/027,839
FILING DATE: SEPTEMBER 30, 1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/012,689
FILING DATE: FEBRUARY 27, 1996
CLASSIFICATION NUMBER: 60/012,689
ATTOMERA/AGENT INFORMATION:
ATTOMERY/AGENT INFORMATION:
TELEPRANCE CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REGISTRATION NUMBER: 39,132
RELEPRANCE (650) 845-4166
INFORMATION FOR SEQ ID NO: 2841:
SEQUENCE CHARACTERISTICS:
LENGTH: 271 base pairs
TYBER INCLEIC acid
STRANDEDRESS: single
 100.0%; Pred. ...
 , Application US/09540208
CURRENT APPLICATION DATA:
 Conservative
 TYPE: DNA
ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
Matches 218; Conserv
 IMMEDIATE SOURCE:
CLONE: 1794787
 US-08-941-869A-2841
 61
 121
 FEATURE:
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 121 GTTCTCAGGTTCTGGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCG 180
 48 CCCAATGCCCCAGCTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAAT 107
 108 TCGCAACCTGCTGGGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGT 167
 168 GITCTCAGGITCTGGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGATTGTCAAGCG 227
 9
 APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Medbecone, Angelo M.
APPLICANT: Naughton, Rebecone E.
APPLICANT: Ringler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: HUMAN PROSTATE
NUMBER OF SEQUENCES: 5486
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALLFORNIA
 1 CCCAATGCCCCAGCTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAAT
 APPLICANT: Delegeme, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF GASTROINTESTINAL SYSTEM TISSUE FILE REPERBACE: DOLYNUCLEOTIDES OF GASTROINTESTINAL SYSTEM TISSUE CURRENT APPLICATION NUMBER: US/09/540,766
CURRENT APPLICATION DATA removed - refer tp PALM or File Wrapper NUMBER OF SEQ ID NOS: 77960
SEQ ID NO 8633
LENGTH: 264
 Gaps
 ö
 Query Match 82.8%; Score 226; DB 24; Length 264; Best Local Similarity 100.0%; Pred. No. 6.4e-51; Matches 226; Conservative 0; Mismatches 0; Indels (
 228 GCGGGTCCCAGGCCTGCACCAGCTCACGTTTCCTTCAG 273
 181 GCGGGTCCCAGGCCTGCAGCTCACCAAGCTACGTTTCCTTCAG 226
 ZIP: 94304
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
 ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu00958497
US-09-540-766-8863
 Sequence 2841, Application US/08941869A GENERAL INFORMATION:
 Sequence 8863, Application US/09540766
GENERAL INFORMATION:
 Gooding, Douglas H.
 Seilhamer, Jeffrey J.
 ORGANISM: Homo sapiens
 US-08-941-869A-2841
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Gaps

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61 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAAAATTCGCAACCTGCTG 120
 APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Sellhamer, Jeffrey J.
APPLICANT: Stuart, Sulan G.
APPLICANT: Stuart, Stuar G.
APPLICANT: Stuart, Stuar G.
APPLICANT: Stuart, Stuar G.
APPLICANT: Will and G.
APPLICANT: Mundhidah, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF HEMIC AND IMMUNE SYSTEM TISSUE
TITLE OF INVENTION: POLYNUCLEOTIDES OF HEMIC AND IMMUNE SYSTEM TISSUE
CURRENT FILING DATE: 2000-03-31
PRIOR PAPLICATION NUMBER: 09/008,119
PRIOR PAPLICATION NUMBER: 09/008,119
PRIOR PILING DATE: 1998-01-16
PRIOR PELING DATE: 1992-11-19
PRIOR APPLICATION NUMBER: 07/916,491
PRIOR APPLICATION NUMBER: 08/438,571
PRIOR PILING DATE: 1994-07-28
PRIOR PELING DATE: 1994-07-28
PRIOR PELING DATE: 1994-07-28
PRIOR PELING DATE: 1994-07-14
PRIOR PELING DATE: 1994-07-14
PRIOR PILING DATE: 1994-07-14
PRIOR PELING DATE: 1994-07-14
PRIOR PILING DATE: 1994-01-11
PRIOR PILING DATE: 1994-01-11
PRIOR PILING DATE: 1995-07-20
 1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCCTTCCCCCAATGCCCCAG
 25 ArdeAdcActAcceeAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG
 121 GGGTTGGCTCTGGGTTGGAGGGCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT
 Gaps
 ö
 77.7%; Score 212; DB 9; Length 245; 98.1%; Pred. No. 4.1e-47; ive 0; Mismatches 4; Indel8
 181 GGCAGGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAG 216
 205 GGCAGGGCTGCAGGAAAGGCTGTCAGNTGCGCTGAG 240
 FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00448643
 ; Sequence 126181, Application US/09540233D; GENERAL INFORMATION:
 NAME/KEY: unsure
LOCATION: 103, 105, 178, 231
 Matches 212; Conservative
 TYPE: DNA
ORGANISM: Homo sapiens
 ; IMMEDIATE SOURCE:
; CLONE: P-033488
US-08-438-571A-2389
 Query Match
Best Local Similarity
 US-09-540-233D-126181
 MOLECULE TYPE:
 SEQ ID NO 126181
 g
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 54 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 113
 61 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG 120
 GGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 180
 233
 174 dddrrddcrcrddcrcddrrddaddcdccacarcrcdcarardradrarcrcaddrrcr
 1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGGGGCCTTCCCCAATGCCCCAG
 Gaps
 APPLICANT: Delegeane, Angelo M.
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Levine, Wendy B.
APPLICANT: Levine, Wendy B.
APPLICANT: Levine, Wendy B.
APPLICANT: Freitas, Nicole
APPLICANT: Jernigan-Kelleher, Colleen
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Pham, Mino Thu
APPLICANT: Bills, Pamela Kay
APPLICANT: Alle, Christina M.
APPLICANT: Aleublom, Ingrid Erika
APPLICANT: Aleublom, Ingrid Erika
TITLE OF INVENTION: POLYUCLEOTIDES DERIVED FROM THP-1 CELLS
NUMBER OF SEQUENCES: 5094
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STREET: STATE: CALIFORNIA
COUNTRY: USA
 ó
 Length 271;
 0; Indels
 ZUDINGRY: USAN
ZID: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
CLASSIFICATION NUMBER: US/08/438,571A
FILING DATE:
CLASSIFICATION: MICHAEL C., Ph.D.
REGISTRATION NUMBER: 39132
REGISTRATION UNMBER: PD-001-5 US
FEGIOWAUNICATION INFORMATION:
TELEPHONE: (415) 855-0555
TELEPAX: (415) 845-4166
INFORMATION FOR SEQ ID NO: 2389:
SEQUENCE CHARACTERISTICS:
TENTATION FOR SEQ ID NO: 2389:
TENTATION FOR SEQ ID NO: 2389:
 181 GGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGAT 218
 234 GGCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAGAT 271
 Query Match
79.9%; Score 218; DB 24;
Best Local Similarity 100.0%; Pred. No. 9.7e-49;
Matches 218; Conservative 0; Mismatches 0;
// NAME/KEY: misc feature
// OTHER INFORMATION: Incyte ID No: hu00317250
US-09-540-208-35269
 LENGTH: 245 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 linear
 TOPOLOGY:
 121
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 108
 49 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 108
 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG 120
 CTACCTCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG 168
 121 GGGTTGGCTCTGGGTCGGTTGGAGGCCGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 180
 GGGTTGGCTTCGGTTGGAGGCCGCAGTGCTCGCCATGTAGTGTTCTCAGGTTCT 180
 49 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG
 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG
 1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCCTTCCCCAATGCCCCAG
 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG
 Gaps
 Gaps
 APPLICANT: Selhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Start, Susan G.
APPLICANT: Sture, Laura L.
APPLICANT: Sture, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara L.
APPLICANT: Mullahy, Sara L.
APPLICANT: Mullahy, Sara L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Sture, Laura J.
APPLICANT: Sture, Laura J.
APPLICANT: Sture, Laura J.
APPLICANT: Sture, J.
APPLICANT: J.
APPLICANT: Sture, J.
APPLICANT: Sture, J.
APPLICANT: Sture, J.
APPLICANT: Sture, J.
APPLICANT: Laura J.
APPLICANT: Sture, J.
APPLICANT: Laura J.
APPLICANT: J.
APPLICANT: Sture, J.
APPLICANT: J.
AP
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 Length 260;
 0; Indels
 75.5%; Score 206; DB 23; Length 2
100.0%; Pred. No. 1.8e-45;
ive 0; Mismatches 0; Indels
 75.5%; Score 206; DB 14;
100.0%; Pred. No. 1.8e-45;
iive 0; Mismatches 0;
 ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: hu00887627
US-09-539-334-6888
 GGCAGGGCTGCAGGAAAGGCTGTCAG 206
 181 GGCAGGCTGCAGGAAAGGCTGTCAG 206
 GGCAGGCTGCAGGAAAGGCTGTCAG 254
 Query Match
Best Local Similarity 100.0
Matches 206; Conservative
 Query Match
Best Local Similarity 100.(
Matches 206; Conservative
 TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
) MOLECULE TYPE: CDN)
; IMMEDIATE SOURCE:
; CLONE: 2071192H2
US-08-959-395-768
 TOPOLOGY: linear
 181
 61
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 109
 121
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 CTACCTCCTGATACCTTINANATGCGGGTCCGAGATGGCAGCAAATTCGCAACCTGCTG 144
 61 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG 120
 121 GGGTTGGCTCTGGGTCGGTTGGAGGCCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 180
 145 GGGTTGGCTCTGGGTTGGAGGCCGCAGTNCTCGGCATGTAGTGTTCTCAGGTTCT 204
 APPLICANT: Gooding, Douglas H.
APPLICANT: Gooding, Douglas H.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura L.
APPLICANT: Ito, Laura G.
APPLICANT: Houghton, Rebeca E.
APPLICANT: Naughton, Rebeca E.
APPLICANT: PALO ALTO
STREET: 3174 PORTER DRIVE
COUNTRY: USA
ZIP.
 1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 60
 25 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 84
 Gaps
 ö
 Length 245;
 4; Indels
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/959,395
FILING DATE: US/08/959,395
FILING DATA:
APPLICATION NUMBER: GO/033,551
FILING DATE: DECEMBER 20, 1996
ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PD-0259 US
TELECOMMUNICATION:
TELECOMMUNICATION:
 GCCAGGCTGCAGGAAAGGCTGTCAGCTGCGCTGAG 216
 205 GGCAGGGCTGCAGGAAAGGCTGTCAGNTGCGCTGAG 240
 77.7%; Score 212; DB 24; 98.1%; Pred. No. 4.1e-47; tive 0; Mismatches 4;
g, or other
 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
 (650) 855-0555
 Floppy disk
; OTHER INFORMATION: a, t, c, US-09-540-233D-126181
 TELEFAX: (650) 845-4166 INFORMATION FOR SEQ ID NO:
 260 base pairs
nucleic acid
EDNESS: single
 Query Match
Best Local Similarity 98.13
Matches 212; Conservative
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
 TYPE: nucleic
STRANDEDNESS:
 181
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60 ATGGAGCACTACCGGANAGCTGGCTCTNTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 119
 61 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGAAATTCGCAACCTGCTG 120
 180 dddriddcrcrdddrddarddadddddacrccdcardrargrarrcrcaddrrcr 239
APPLICANT: Gooding, Douglas H.
APPLICANT: Gooding, Douglas H.
APPLICANT: Stuve, Laura L.
APPLICANT: Stuvet, Susan G.
APPLICANT: Ito, Laura L.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Maughton, Rebecca E.
APPLICANT: Maughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM NUMBER OF SEQUENCES: 7797
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PITTLE OF STURE AND POLYPEPTIDES DERIVED FROM STURE OF INVENTION: HUMAN BRAIN
NUMBER OF SEQUENCES: 7797
STURE OF INVENTION: HUMAN PRAIN
NUMBER OF SEQUENCES: 7797
STURE OF INVENTE AND POLYPEPTIDES DERIVED FROM NUMBER OF SEQUENCES: 7797
STURE OF INVENTION: HUMAN BRAIN
NUMBER OF SEQUENCES: 7797
STURE OF INVENTE AND POLYPEPTIDES DERIVED FROM NUMBER OF SEQUENCES: 7797
 120 CTACCTCCTGATACCCTTNANATGCGGGTCCGAGATGGCAGCAGCAAATTNGCAACCTGCTG
 1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG
 Query Match 71.8%; Score 196; DB 14; Length 262; Best Local Similarity 97.5%; Pred. No. 9.5e-43; Matches 196; Conservative 0; Mismatches 5; Indels
 COUNTEXT: USAR
ZIP: 9430A
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,620
FILING DATE: HEREWITH
CLASSIFICATION DATA:
PILING DATE: DECEMBER 6,1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 60/032,151
FILING DATE: MARCH 7, 1997
CLASSIFICATION: 536
APPLICATION NUMBER: 08/812,505
FILING DATE: MARCH 7, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
TELEPHONE: (650) 852-0195
INFORMATION FOR SEQ ID NO: 1415:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 ; Sequence 1415, Application US/08978620 ; GENERAL INFORMATION:
 STREET: 3174 PORTER CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA
 MOLECULE TYPE: CD
IMMEDIATE SOURCE:
CLONE: 862319
 US-08-978-620-1415
 US-08-978-620-1415
 121
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 60 ATGGAGCACTACCGGANAGCTGGCTCTNTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 119
 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG 120
 121 GGGTTGGCTCTGGGTTGGAGGGCGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 180
 239
 APPLICANT: Gooding, Douglas H.
APPLICANT: Guara L.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura L.
APPLICANT: Ito, Laura Y.
APPLICANT: Acrblom, Ingrid E.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Naughton, Rebeca E.
APPLICANT: Klingler, Tod M.
ITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM ITLE OF INVENTION: SATROCYTOMA
NUMBER OF SEQUENCES: 3896
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACHTOMA
 1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG
 120 ciacciccidaracccirmanardcodorccoadarodcadaranimocaacciocio
 Gaps
 ó,
 Query Match
71.8%; Score 196; DB 13; Length 262;
Best Local Similarity 97.5%; Pred. No. 9.5e-43;
Matches 196; Conservative 0; Mismatches 5; Indels
 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,505
FILING DATE:
 STREET: 3174 PORTER BRAMACEUTICALS, INC. STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CALIFORNIA COUNTRY: USA
 GGCAGGCTGCAGGAAAGGCT 201
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/013,529
 ATTORNEY AGENT INFORMATION:
NAME: LUTHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PD-01.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 855-0195
INFORMATION FOR SEQ ID NO: 1415:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
 MOLECULE TYPE: CDNA IMMEDIATE SOURCE: CLONE: 862319
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 FILING DATE:
 US-08-812-505-1415
 US-08-812-505-1415
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APPLICANT: Stuv , Laura L.
APPLICANT: Stuv , Laura B.
APPLICANT: Ito, Laura W.
APPLICANT: Averblom, Ingrid E.
APPLICANT: Maughton, Rebeca E.
APPLICANT: Maughton, Rebeca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM HUMAN TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM HUMAN TITLE OF INVENTION: POLYNUCLEOTIDES AND SEQUENCES: 5970
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
 60 Argeadcacracceganaecreecrerrragaecreccaececrreccaarecceae 119
 61 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG 120
 120 CTACCICCIGATACCCTITNANATGCGGGTCCGAGATGCCAGCAAAATTNGCAACCTGCTG 179
 121 GGGTTGGCTCTGGGTCGGTTGGAGGGCGCAGGTCGCCATGTAGTGTTCTCAGGTTCT 180
 180 GGGTTGGCTCTGGGTCGGTTGGAGGCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 239
 1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 60
 Gaps
 ö
 Length 262;
 5; Indels
 COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYTEM:
OPERATING SYTEM:
OPERATING SYTEM:
OPERATING SYTEM:
OPERATING DATE:
CLASSIFICATION NUMBER: US/60/013,529
FILING DATE:
NAME: UNTHER, BARBARA J.
REGISTRATION NUMBER: 33954
REFERENCE/DOCKET NUMBER: PD-0126P
TELECOMMUNICATION NUMBER: PD-0126P
TELECOMMUNICATION NUMBER: PD-0126P
TELECOMMUNICATION NUMBER: PD-0126P
TELECOMMUNICATION NUMBER: GS-0555
TELECOMMUNICATION NO: 1415:
SEQUENCE CHARACTERISTICS:
LENGTH: 262 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
CLONE: 862319
 71.8%; Score 196; DB 66; 97.5%; Pred. No. 9.5e-43; tive 0; Mismatches 5;
 Sequence 5067, Application US/08951197; GENERAL INFORMATION:
 GGCAGGCTGCAGGAAAGGCT 201
 240 GCCAGGCTGCAGGAAAGGCT 260
3174 PORTER DRIVE
 Query Match 71.8
Best Local Similarity 97.5
Matches 196; Conservative
 PALO ALTO
CALIFORNIA
 CITY: PALO STATE: CALI COUNTRY: US ZIP: 94304
 US-60-013-529-1415
 US-08-951-197-5067
 181
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 8
 CTACCTCCTGATACCCTTNANATGCGGGTCCGAGATGGCAGCAAAATTNGCAACCTGCTG 179
 60 ATGGAGCACTACCGGANAGCTGGCTCTNTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 119
 61 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG 120
 121 GGGTTGGCTCTGGGTCGGTTGGAGGGCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 180
 180 GGGTTGGCTCTGGGTTGGAGGCCGCCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 239
 Sequence 45100. Application US/09540229
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Mullahy, Sara J.
APPLICANT: Wullahy, Sebecca B.
TITLE OF INVENTION: POLYNUCLEOTIDES OF NERVOUS SYSTEM AND SENSORY ORGANS FILE REFERENCE: PD-1033 CIP
CURRENT PILING DATE: 2000-03-13
Prior application data removed - refer to PALM or file wrapper NORWARD POSTERIAL OF SEQ. ID NOS: 193582
 1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG
 Gaps
 APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuart, Susan G.
APPLICANT: Ito, Laura Y.
APPLICANT: Akerblom, Ingrid E.
APPLICANT: Medegeane, Angelo M.
APPLICANT: Mughton, Rebecca E.
APPLICANT: Klingler, Tod M.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM TITLE OF INVENTION: ASTROCYTOMA
NUMBER OP SEQUENCES: 3896
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
 ;
0
 71.8%; Score 196; DB 24; Length 262; 97.5%; Pred. No. 9.5e-43;
 Indels
 0; Mismatches
 NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu00691274
NAME/KEY: unsure
LOCATION: 38, 76, 87, 138, 140, 168
OTHER INFORMATION: a, t, c, g, or other
 Sequence 1415, Application US/60013529
GENERAL INFORMATION:
APPLICANT: Gooding, Douglas H.
 240 GCCAGGCTGCAGGAAAGGCT 260
 GGCAGGGCTGCAGGAAAGGCT 201
 Query Match
Best Local Similarity 97.57
Matches 196; Conservative
 SOFTWARE: PERL Program
SEQ ID NO 45100
LENGTH: 262
 TYPE: DNA
ORGANISM: Homo sapiens
 US-09-540-229-45100
 US-09-540-229-45100
 US-60-013-529-1415
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 181
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Gaps

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58 ArdGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCCAATGCCCCAG 117
 121 GGGTTGGCTCTGGGTCGGTTGGAGGCCGCAGGTCGTCGGCATGTAGTGTTCTCAGGTTCT 180
 61 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGAAAATTCGCAACCTGCTG
 US-09-539-806B-30498

Sequence 3049B, Application US/09539806B

Sequence 3049B, Application US/09539806B

Sequence 3049B, Application US/09539806B

APPLICANT: Sellhamer, Jeffrey J.

APPLICANT: Stude, Laura L.

APPLICANT: Stude, Laura L.

APPLICANT: Stude, Laura L.

APPLICANT: Maughton, Rebecca E.

TILLE OF INVENTION: POLYNUCLEOTIDES OF EXOCRINE GLAND TISSUE

TILLE OF INVENTION: POLYNUCLEOTIDES OF EXOCRINE GLAND TISSUE

CURRENT APPLICATION UNUBER: US/09/539,806B

CURRENT APPLICATION NUMBER: 08/706,766

PRIOR PLING DATE: November 15, 1996

PRIOR PLING DATE: November 15, 1996

PRIOR PLING DATE: November 15, 1996

PRIOR PLING DATE: March 20, 1997

PRIOR PLING DATE: March 20, 1997

PRIOR PLING DATE: March 20, 1997

PRIOR PLING DATE: Warch 20, 1997

PRIOR PLING DATE:
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FILE REFERENCE: PD-1027 CIP
CURRENT APPLICATION NUMBER: US/09/539,806
CURRENT FILING DATE: 2000-03-30
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 48372
SOFTWARE: PERL PROGRAM
 Length 250;
 Indels
 Query Match 70.7%; Score 193; DB 23; I Best Local Similarity 100.0%; Pred. No. 6.2e-42; Matches 193; Conservative 0; Mismatches 0;
 NAMEXES: misc feature
; OTHER INFORMATION: Incyte ID No: hu00555791
US-09-539-806-30498
 238 GGCAGGGCTGCAG 250
 181 GGCAGGCTGCAG 193
 TYPE: DNA
ORGANISM: Homo sapiens
 SEQ ID NO 30498
LENGTH: 250
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 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG 120
 121 GGGTTGGCTCTGGGTCGGTTGGAGGCCGGCAGTGCTCGGCATGTAGTGTTCTCAGGTTCT 180
 58 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG
 1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGGGGCCTTCCCCAATGCCCCAG
 CTACCTCCTGATACCCTTGAGATGCGGGTCCGAGATGGCAGCAAAATTCGCAACCTGCTG
 Gaps
 °,
 70.7%; Score 193; DB 14; Length 250; 100.0%; Pred. No. 6.2e-42; ive 0; Mismatches 0; Indels
 APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Naughton, Rebecca E.
TITLE OF INVENTION: POLYNUCLEOTIDES OF EXOCRINE GLAND TISSUE
 MEDIUM TYPE: Floppy disk
COMPUTER: ELoppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
FILING DATE: WORDER: 60/027,249
FILING DATE: OCTOBER 1, 1996
CLASSIFICATION NUMBER: 08/826,438
FILING DATE: MARCH 20, 1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/822,285
FILING DATE: MARCH 20, 1997
CLASSIFICATION NUMBER: 08/822,285
FILING DATE: MARCH 20, 1997
 ATTORNEY/AGENT INFORMATION:
NAME: CERRONE, MICHAEL C.
REGISTRATION NUMBER: 39 132
REFERENCE/DOCKET NUMBER: PD-0143-1 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0556
INFORMATION FOR SEQ ID NO: SGOT:
SEQUENCE CHARACTERISTICS:
LENGTH: 250 base pairs
TYPE: nucleic acid
STRANDEDNES: single
 Sequence 30498, Application US/09539806
GENERAL INFORMATION:
APPLICANT: Seilhamer, Jeffrey J.
APPLICANT: Delegeane, Angelo M.
APPLICANT: Stuart, Susan G.
APPLICANT: Stuve, Laura L.
 GGCAGGGCTGCAG 193
 Query Match
Best Local Similarity 100.
Matches 193; Conservative
 ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
 linear
 ; IMMEDIATE SOURCE:
; CLONE: 1997229
US-08-951-197-5067
 TOPOLOGY: 11
MOLECULE TYPE:
 US-09-539-806-30498
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58 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 117
 1 ATGGAGCACTACCGGAAAGCTGGCTCTGTAGAGCTCCCAGCGCCTTCCCCAATGCCCCAG 60
 0; Gaps
 Query Match 70.7%; Score 193; DB 23; Length 250; Best Local Similarity 100.0%; Pred. No. 6.2e-42; Matches 193; Conservative 0; Mismatches 0; Indels (
; SEQ ID NO 30498
; LENGTH: 250
; TYPE: DNA
; CGANISM: HOMO Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: hu00555791
US-09-539-8068-30498
 Search completed: January 31, 2005, 20:58:10 Job time : 2461 secs
 181 GGCAGGGCTGCAG 193
 238 GGCAGGCTGCAG 250
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Sequence 15214, Application US/09513999C

Sequence 15214, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:
APPLICANT: Duclert, A. APPLICANT: Duclert, A. APPLICANT: Gooded Human Proteins.
APPLICANT: Gooded J.Y.

TILLO OF 193961

FILE REFERENCE: 59.US2.REG

CURRENT FILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/122,487
 US-09-513-999C-15513/c
 RESULT 2
US-09-513-999C-15214/c
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 Sequence 24985, A. Sequence 15004, A. Sequence 1319, A. Sequence 1316, A. Sequence 1316, A. Sequence 1518, A. Sequence 15287, A. Sequence 1500, A. Sequence 1500, A. Sequence 1500, A. Sequence 27, Appl. Sequence 27, Appl. Sequence 227, Appl. Sequence 217, Appl. Sequence 217, Appl. Sequence 1517, Appl. S
 Sequence 2, Appli
Sequence 2, Appli
 January 31, 2005, 21:02:13 ; Search time 68 Seconds (without alignments) 1285.692 Million cell updates/sec
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/Aa_COMB.seq:*
/cgn2_6/ptodata/1/ina/Ra_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
 US-09-513-999C-15513

US-09-513-999C-15214

US-09-513-999C-24985

US-09-513-999C-24985

US-09-513-999C-3433

US-09-513-999C-3433

US-09-513-999C-14651

US-09-513-999C-14651

US-09-513-999C-15287

US-09-513-999C-15287

US-09-513-999C-15605

US-09-513-999C-15605

US-09-513-999C-15605

US-09-513-999C-15605

US-09-513-996-15605

US-09-613-618-62

US-09-618-618-62

US-09-705-1575

US-09-705-1575

US-09-705-1575

US-09-705-1575

US-09-618-81575

US-09-618-81575

US-09-618-81575

US-09-618-81575
 Total number of hits satisfying chosen parameters:
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US-08-828-712-2
US-09-063-276-2
 824507 segs, 355394441 residues
 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
 - nucleic search, using sw model
 IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
 Issued Patents NA:*
 Query
Match Length
 Minimum DB seq length: 0
Maximum DB seq length: 123
 18.8
18.6
18.6
 Scoring table:
 Perfect score:
 OM nucleic
 Sequence:
 Searched:
 Run on:
 Result
No.
```

```
Sequence 15513, Application US/09513999C

Fatent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dunas Milne Edwards, J.B.

APPLICANT: Dunclert, A.

APPLICANT: Duclert, A.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REFERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT PILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 15513

LENGTH: 89
 60 GCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGGTGCTGCTCAGCCGGGA 119
 70 GCTCGTCCCGCGTGCGCCAGCCGCCGCCGCTGCTGCTGCTGCTGCTCCTCCTCCGGAT 11
 Gape
 Sequence
Sequence
Sequence
 Sequence 3
Sequence 3
Sequence 3
 Sequence
Sequence
Sequence
 Sequence
 Sequence 3
Sequence 1
Sequence 2
 Sequence
 ö
 Query Match 18.7%; Score 23; DB 4; Length 89; Best Local Similarity 60.3%; Pred. No. 1.8e+02; Matches 38; Conservative 0; Mismatches 25; Indels
US-09-324-782-2
US-09-668-143-2
US-08-952-73-176
US-09-913-990C-20555
US-09-131-990C-20555
US-09-513-990C-20555
US-09-999-672-20
US-08-999-672-20
US-08-999-672-20
US-08-190-802A-20
US-08-190-802A-20
US-08-190-802A-20
US-08-130-990C-35019
US-08-131-999C-35019
US-09-513-999C-35019
US-09-513-999C-35019
US-09-513-999C-35019
 ALIGNMENTS
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-15513
```

```
COUNTRY:
 STREET:
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 APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
PILE REFERENCE: 59.US2.REG
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR PILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 15004
LENGTH: 66
 Gaps
 Gaps
 69 CCTCACAGTGCGCCGCCATGTGCCTGCAGTGGTGGTGCTGCTCAGCCGGGACCCC 123
 76 CATGAACGTGGGCAGGAAAGCGGCTGCAATGCTGGGCTGTTCTGCATGGAGCGC 22
 Score 21.4; DB 4; Length 119;
Pred. No. 6.1e+02;
0; Mismatches 21; Indels
 16.7%; Score 20.6; DB 4; Length 77; 74.3%; Pred. No. 1e+03; tive 0; Mismatches 9; Indels
 26 AGGACAGCTGGGTCCCAGCCTCACCTGACACAGGG 60
 32 AGGACTICITGGITTCAGCATAACCTAAGACAGGG 66
 S-09-513-999C-15004/c
Sequence 15004, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
 Query Match
Best Local Similarity 61.8%;
Matches 34; Conservative
PRIOR FILING DATE: 1999-02-26
 NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
 Query Match
Best Local Similarity 74.3'
Matches 26; Conservative
 TYPE: DNA
CAGANISM: Homo sapiens
US-09-513-999C-15214
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-24985
 ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-15004
 RESULT 3
US-09-513-999C-24985
 SEQ ID NO 15214
LENGTH: 119
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```

```
Sequence 13, Application US/08120324

Patent No. 6723556

GENERAL INFORMATION:
APPLICANT: Saxena, Brij B.
APPLICANT: Rathnam, Premila
ITILE OF INVENTION: RECEPTOR AND hCG-hLH
TITLE OF INVENTION: RECEPTOR-hCG COMPLEX AS ANTIGENS, ANTIBODIES THERETO AND INVENTION: CONTRACEPTIVE VACCINE
INTHER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
 94
 65 dérieccideaireréirréacaereaceaecréacaireacedecréecréere
 35 GGGTCCCAGCCTCACCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTG
 Gaps
 ..
0
 Length 66;
 Score 20.4; DB 4; Length 6
Pred. No. 1.1e+03;
0; Mismatches 26; Indels
 COMPUTER: PLODPY disk
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC compatible
COMPUTER: PEN PC-DOS/MS-DOS
COMPUTER: PEN PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: PATENTING SYSTEM: US/08/120,324
FILING DATE: 14-SEP-1993
CLUASSIFFCATION: DATA:
APPLICATION NUMBER: US 08/029,613
FILING DATE: 11-MAR.1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/879,245
FILING DATE: 06-MAY.1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/742,236
FILING DATE: 23-JUL-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/910,554
FILING DATE: 23-JUL-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/910,554
FILING DATE: 08-JUL-1985
PRIOR APPLICATION NUMBER: US 06/752,497
FILING DATE: 08-JUL-1985
PRIOR APPLICATION NUMBER: US 06/752,497
FILING DATE: 02-DEC-1982
ATPONDEY/AGENT INFORMATION:
NAMME: NAKAMILTA
 E: SUGHRUE, MION, ZINN, MACPEAK & SEAS 2100 Pennsylvania Avenue, N.W.
 NAME OF THE PROBLEM OF T
Query Match
Best Local Similarity 58.1%;
Matches 36; Conservative
 INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
TENGTH: 90 base pairs
 TYPE: nucleic acid
STRANDEDNESS: single
 CITY: Washington
 95 CA 96
 GA
4
 US-08-120-324-13
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13. 3 rd.

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RESULT 8
US-09-513-999C-14651
j Sequence 14651, Application US/09513999C
j Sequence 14651, Application US/09513999C
j Retent No. 6703961
j GENERAL INFORMATION:
j APPLICANT: Duclas Milne Edwards, J.B.
j APPLICANT: Duclast, A.Y.
j APPLICANT: Glordano, J.Y.
j TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
j Patent No. 6703961
j FILE REFERENCE: 59.U82.REG
j CURRENT FILING DATE: 200-02-24
j PRIOR PILING DATE: 1999-02-26
j NUMBER OF SEQ ID NOS: 36681
j SEQ ID NO 14651
j LENGTH: 112
 Sequence 25968, Application US/09513999C
; Sequence 25968, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Duclart, A.
; APPLICANT: Duclart, A.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 1909-02-24
; PRIOR PILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 25968
; LENGTH: 92
44 CCGGAGATGGCGGGGGTGCTGAACGCAGAGCGACTCGAGGTGTCCGTCGACGGCCTCACG 103
 48 AGACTICAGGAGACCARAGCCCAGCTIGCCAGGCACTGAGCTAGAAGCCCTGCCATGGC 107
 20 AGACTGAGGACAGCTGGGTCCCAGCCTCACCTGACACAGGGCTAGACCCCCTCACAGTGC 79
 Gape
 ö
 16.1%; Score 19.8; DB 4; Length 112; 55.4%; Pred. No. 1.9e+03;
 Indele
 1; Mismatches
 NAME/KEY: misc_feature
LOCATION: 6
OTHER INFORMATION: h=a or c or t
 104 crcadcccddacc 116
 109 CTCAGCCGGGACC 121
 36; Conservative
 OTHER INFORMATION: rea or
 TYPE: DNA ORGANISM: Homo sapiens
 TYPE: DNA
ORGANISM: Homo sapiens
 NAME/KEY: misc_feature
 Best Local Similarity
Matches 36; Conserv
 108 AČĆCĆ 112
 80 GCCGC 84
 US-09-513-999C-25968
 US-09-513-999C-14651
 LOCATION: 65
 Query Match
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 Sequence 13916, Application US/09513999C

Sequence 13916, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dumas Mine Edwards, J.B.

APPLICANT: Ducert, A.

APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PATENT: APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

PATENT: PAPLICATION NUMBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US 60/122,487

PRIOR PAPLICATION NUMBER: US 60/122,487

PRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SEQ ID NO 13916

TENNOM: APPLICATION NOS: 36681

SEQ ID NO 13916
 Sequence 34339, Application US/09513999C
; Sequence 10. 6783951
; Retent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Dunas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REPERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT PELING DATE: 1999-02-24
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 33439
; LENGTH: 106
 Gaps
 Gaps
 67 CCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTGCTGCTCAGCCGGGAC 120
 ;
0
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 ;
0
 72 CACAGTGCGCCGCCATGTGCCTGCAGTGTGGTGCTGCTCAGCCGGGAC 120
 46 ccceccecececcrecicacedadadecreciacicerecientes
 Query Match
16.4%; Score 20.2; DB 4; Length 106;
Best Local Similarity 63.3%; Pred. No. 1.4e+03;
Matches 31; Conservative 0; Mismatches 18; Indels 0
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16.4%; Score 20.2; DB 4; Length 116;
Best Local Similarity 54.8%; Pred. No. 1.5e+03;
Matches 40; Conservative 0; Mismatches 33; Indels
 16.6%; Score 20.4; DB 4; Length 90; 61.1%; Pred. No. 1.2e+03; Live 0; Mismacches 21; Indels
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-120-324-13
 Query Match
Best Local Similarity 61.19
Matches 33; Conservative
 ; ORGANISM: Homo sapiens
US-09-513-999C-33439
 ; ORGANISM: Homo sapiens
US-09-513-999C-13916
 US-09-513-999C-33439
 US-09-513-999C-13916
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49 CCTGACACAGGGCTAGACCCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTTGTTG 108

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FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
FRIOR APPLICATION NUMBER: US 60/122,487
FRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 15605
LENGTH: 103
 Conservative
 ; ORGANISM: Homo sapiens
US-09-513-999C-15605
 Query Match
Best Local Similarity
Matches 34; Conserv
 Query Match
Best Local Similarity
Matches 29; Conserv
 US-09-985-357A-7/c
 US-09-463-380-7/c
 FEATURE:
NAME/KEY: CDS
 TYPE: DNA
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 ö
 Sequence 15287, Application US/09513999C

| Sequence 15287, Application US/09513999C
| Patent No. 6783961
| APPLICANT: Dumas Milne Edwards, J.B.
| APPLICANT: Dumas Milne Edwards, J.B.
| APPLICANT: Dumas Milne Edwards, J.B.
| APPLICANT: Giordano, J.Y.
| TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| PATENT APPLICATION UNMBER: US/09/513,999C
| CURRENT FILING DATE: 2000-02-24
| PRIOR APPLICATION NUMBER: US 60/122,487
| PRIOR FILING DATE: 1999-02-26
| WUMBER OF SEQ ID NOS: 36681
| SCPTWARE: Patent.pm
| SEQ ID NO 15287
 66 CCCCTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTGCTGGTCAGCCGGGAGCCC 123
 ccccraccrrcccaaarticraacrrcaaarricaaccrcrcaccaccaccaccacc
 Gaps
 US-09-513-999C-15605/c

Sequence 15605, Application US/09513999C

Patent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Glordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961
 0; Gaps
 ö
 75 AGTGCGCCGCCATGTGCCTGCAGTGTGGGTGCTGCTCAGCCGGGACCC 122
 i; DB 4; Length 92;
2.2e+03;
thes 18; Indels
 Score 19.6; DB 4; Length 103;
Pred. No. 2.2e+03;
0; Mismatches 24; Indels
 Score 19.6; DB
Pred. No. 2.2e+
1; Mismatches
 ; OTHER INFORMATION: v=a or c or US-09-513-999C-25968
 Query Match
Best Local Similarity 60.4%;
Matches 29; Conservative
 15.9%;
58.6%;
 FEATURE:
NAME/KEY: misc_feature
LOCATION: 8
OTHER INFORMATION: n=a, g,
 ; OTHER INFORMATION: k=g or t
US-09-513-999C-15287
 Conservative
 NAME/KEY: misc_feature
LOCATION: 7
OTHER INFORMATION: n=a,
 NAME/KEY: misc_feature
LOCATION: 9
 TYPE: DNA
ORGANISM: Homo sapiens
 OTHER INFORMATION: k=g
 NAME/KEY: misc_feature LOCATION: 2
 NAME/KEY: misc_feature
 Query Match
Best Local Similarity
Matches 34; Conserv
 US-09-513-999C-15287/c
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 g
 ð
 셤
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```
; Sequence 7, Application US/09463380; Patent No. 6391633; Ratent No. 6391633; GENERAL INFORMATION: FAPLICANT: Anne STERN; Michael BRANDT; Konrad HONOLD; Johannes AUER; Hans KOLL; TITLE OF INVENTION: Preparation of erythropoietin by endogenous gene activation; FILE REFRENCE: HURR 1151 PFF/MAS; CURRENT APPLICATION NUMBER: US/09/463,380; CURRENT FILING DATE: 2000-01-21; PRIOR APPLICATION NUMBER: PCT/FP98/04590; PRIOR FILING DATE: 1998-07-10; PRIOR FILING DATE: 1998-07-10; PRIOR APPLICATION NUMBER: US 09/113,692; PRIOR APPLICATION NUMBER: EP 97112640; PRIOR APPLICATION NUMBER: EP 97112640; PRIOR FILING DATE: 1997-07-23; PRIOR FILING DATE: Nordperfect 6/7/8
 Sequence 7, Application US/09985357A

Sequence 7, Application US/09985357A

Setent No. 6544748

GENERAL INFORMATION:

APPLICANT: Anne STERN; Michael BRANDT; Konrad HONOLD; Johannes AUER; Hans KOLL

TITLE OF INVENTION: Preparation of erythropoietin by endogenous gene activation

CURRENT APPLICATION NUMBER: US/09/985,357A

CURRENT APPLICATION NUMBER: US/09/985,357A

PRIOR APPLICATION NUMBER: US 09/463,380

PRIOR FILING DATE: 2000-01-21
) LOCATION: 49..60
) OTHER INFORMATION: Nucleotide sequence of the primer EX3 (Met-Gly-Ala-His).
US-09-463-380-7
 ö
 66 CCCCTCACAGTGCGCCCATGTGCCTGCAGTGTGGTGCTGCTCAGCCGGGACCCC 123
 Gaps
 ö
 Length 103;
 15.8%; Score 19.4; DB 3; Length 78; 64.4%; Pred. No. 2.4e+03; Live 0; Mismatches 16; Indels
 70 CTCACAGTGCGCCGCCATGTGCCTGCAGTGTGGGTGCTGCTCAGC 114
 24; Indels
 66 cricacceredecececarecececedesecredeceredesereceredes 22
15.9%; Score 19.6; DB 4;
ilarity 58.6%; Pred. No. 2.2e+03;
Conservative 0; Mismatches 24;
 0; Mismatches
 LENGTH: 78
TYPE: DNA
ORGANISM: Artificial sequence
```

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77 GCCGGATCCGGGCCTCATGTCGAACAGTGCAGCTGAGGCGGACTGCGATCGACTTGAGC 18
 32 GCTGGGTCCCAGCCTCACCTGACACAGGCCTAGACCCCCTCACAGTGCGCCCGTGTGTGC 91
 Gaps
 ö
 15.6%; Score 19.2; DB 2; Length 77; 54.2%; Pred. No. 2.8e+03;
 Sequence 227, Application US/08481710
| Patent No. 6028186
| GENERAL INFORMATION:
| APPLICANT: DIANE TASSET
| APPLICANT: SUMEDHA JAYASENA
| APPLICANT: SUMEDHA JAYASENA
| APPLICANT: LARRY GOLD
| TITLE OF INVENTION: HICH AFFINITY NUCLEIC ACID LIGANDS
| TITLE OF INVENTION: OF CYTOKINES
| NUMBER OF SEQUENCES: 258
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: SARABON and Bratschun, L.L.C.
| STREET: MA00 East Prentice Avenue, Suite #200
 33; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
 0; Mismatches
 SCETAIRS SILENERS
SCETAIRS SILENERS
SCETAIRS SILENERS
SPECIATION NUMBER: US/08/481,710
FILING DATE: 7-UUNE-1995
CLASSIFICATION NUMBER: US/14,131
FILING DATE: 10-UUNE-1991
FILING DATE: 10-UUNE-1991
FILING DATE: 10-UUNE-1991
FILING DATE: 17-AUGUST-1992
FILING DATE: 17-AUGUST-1992
FILING DATE: 17-AUGUST-1992
FILING DATE: 21-OCTOBER-1992
FILING DATE: 21-OCTOBER-1993
FILING DATE: 8-SEPTEMBER-1993
FILING DATE: 8-SEPTEMBER-1993
FILING DATE: 07/564,624
FILING DATE: 17-MINESE: 08/117,991
FILING DATE: 17-MINESE: 08/117,991
FILING DATE: 07-MINESE: 07/564,624
FILING DATE: 08-SEPTEMBER-1993
FRICK APPLICATION NUMBER: 08/117,991
FILING DATE: 07-MINESE: 07/564,428
 REFERENCE/DOCKET NUMBER: NEX1-1
TELECOMUNICATION INPORMATION:
TELEPHONE: (303) 793-3433
TELEPAT: (303) 793-3433
INFORMATION FOR SEQ ID NO: 227:
SEQUENCE CHARACTERISTICS:
LENGTH: 77 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
 33,960
 FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
REGISTRATION NUMBER: 33,960
 92 CTGCAGTGTGGG 103
 39; Conservative
 17 GTTTATTCTGAG 6
 REGISTRATION NUMBER:
 CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
 Best Local Similarity
 US-08-481-710-227/C
 US-08-477-527A-227
 Query Match
 Matches
 셤
 à
 ð
 FEATURE:
NAME/KEY: CDS
LOCATION: 49..60
COTHER INFORMATION: Nucleotide sequence of the primer EX3 (Met-Gly-Ala-His). US-09-985-357A-7
 Gaps
 Sequence 227, Application US/08477527A
Fatent No. 597559
GENERAL INFORMATION:
APPLICANT: DIANE TASSET
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
ITTLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
ITTLE OF INVENTION: OF CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: SAMENGON and Bratschun, L.L.C.
STREET: GAOO East Prentice Avenue, Suite #200
 15.8%; Score 19.4; DB 4; Length 78, 64.4%; Pred. No. 2.4e+03; tive 0; Mismatches 16; Indels
 70 CTCACAGTGCGCCCATGTGCCTGCAGTGTGGGTGCTGCTCAGC 114
 COUNTRY:
ZIP: 80111
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage COMPUTER: IBM compatible COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFFWARE: WORDERECT 6.0
CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/477,527A FILING DATE: 7-UNB-1995
PRIOR APPLICATION DATA: 707/14,131
FILING DATE: 10-UNB-1991
PRIOR APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA: APPLICATION NUMBER: 07/964,624
FILING DATE: 12-OCTOBER-1992
PRIOR APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
 PRIOR FILING DATE: 1998-07-22
PRIOR APPLICATION NUMBER: US 09/113,692
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: DE 19753681.1
PRIOR APPLICATION NUMBER: EP 97112640
PRIOR FILING DATE: 1997-12-03
PRIOR FILING DATE: 1997-07-23
SOFTWARE: Wordperfect
PRIOR APPLICATION NUMBER: PCT/EP98/04590
PRIOR FILING DATE: 1998-07-22
 FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
 TYPE: DNA ORGANISM: Artificial sequence
 Query Match
Best Local Similarity 64.44
Matches 29; Conservative
 STREET: 8400 bcc...
CITY: Denver
STATE: Colorado
 RESULT 14
US-08-477-527A-227/c
 SEQ ID NO 7
```

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```
REFERENCE/DOCKET NUMBER: NEX41-2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TO BE ```